

	10	20	30	40	50	60	70	80	90	100
1	-	-	-	-	-	-	-	-	-	-
human	MRPQGPAA\$PQRRLGI	-----	-----	-----	-----	-----	-----	-----	-----	-----
mouse	MHPQGRAA\$PQ\$LLGFLV\$LLQLSAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPGROGSPGANGIPGTPGIPGRDGFKGEKGECLRESF	-----	-----	-----	-----	-----	-----	-----	-----	-----
rice_fish	MTPLISPR\$LLICLAI\$PLHQE	-----	-----	-----	-----	-----	-----	-----	-----	-----
zebra_fish	MGTKLTLQ\$LLICF\$WISLPP\$C\$V\$TQ\$KAKERI\$P\$Q	-----	-----	-----	-----	-----	-----	-----	-----	-----
chicken	RP\$REVLEAYNGVCLQGP\$SGVPG\$RDG\$NP\$GT\$NG\$IP\$GTP\$GIP\$GRDG\$P\$KGEKGECLRESI	-----	-----	-----	-----	-----	-----	-----	-----	-----
in sensus	...11.....p.....k.....r.....r#v....yng.C1QGP.Gv\$PGRDGNPG.NGIPGTPGIPGRDG.KGEKGECLresf	-----	-----	-----	-----	-----	-----	-----	-----	-----
101	110	120	130	140	150	160	170	180	190	200
1	1	1	1	1	1	1	1	1	1	1
human	EE\$WT\$PNY\$KQ\$CS\$SS\$S1\$NY\$G\$D\$LG\$K\$IA\$E\$C\$T\$F\$K\$M\$R\$S\$N\$S\$A\$R\$V\$L\$F\$S\$G\$S\$L\$R\$K\$C\$R\$N\$A\$C\$C\$Q\$W\$Y\$F\$T\$F\$N\$G\$A\$E\$C\$G\$P\$L\$P\$E\$A\$T\$Y\$T\$D\$Q\$G\$S\$P\$E\$M\$N\$S\$T\$T\$N\$H\$R\$T\$S\$S\$E	-----	-----	-----	-----	-----	-----	-----	-----	-----
mouse	EE\$WT\$PNY\$KQ\$CS\$SS\$S1\$NT\$G\$D\$LG\$K\$IA\$E\$C\$T\$F\$K\$M\$R\$S\$N\$S\$A\$R\$V\$L\$F\$S\$G\$S\$L\$R\$K\$C\$R\$N\$A\$C\$C\$Q\$W\$Y\$F\$T\$F\$N\$G\$A\$E\$C\$G\$P\$L\$P\$E\$A\$T\$Y\$T\$D\$Q\$G\$S\$P\$E\$M\$N\$S\$T\$T\$N\$H\$R\$T\$S\$S\$E	-----	-----	-----	-----	-----	-----	-----	-----	-----
rice_fish	EE\$W\$K\$P\$N\$Y\$K\$Q\$C\$A\$W\$N\$S\$1\$NY\$G\$D\$LG\$K\$IA\$D\$C\$T\$F\$K\$R\$S\$E\$S\$A\$R\$V\$L\$F\$T\$G\$S\$L\$R\$K\$C\$T\$A\$C\$Q\$R\$W\$Y\$F\$T\$F\$N\$G\$A\$E\$C\$T\$G\$E\$L\$P\$V\$E\$S\$T\$Y\$T\$D\$Q\$G\$S\$P\$E\$M\$N\$S\$T\$T\$N\$H\$R\$T\$S\$S\$E	-----	-----	-----	-----	-----	-----	-----	-----	-----
zebra_fish	EE\$W\$K\$P\$N\$F\$K\$Q\$C\$W\$N\$S\$1\$NY\$G\$D\$LG\$K\$IA\$E\$C\$T\$F\$K\$Q\$R\$S\$D\$A\$R\$V\$L\$F\$S\$G\$S\$L\$R\$K\$C\$T\$A\$C\$Q\$R\$W\$Y\$F\$T\$F\$N\$G\$A\$E\$C\$T\$G\$E\$L\$P\$V\$E\$S\$T\$Y\$T\$D\$Q\$G\$S\$P\$E\$M\$N\$S\$T\$T\$N\$H\$R\$T\$S\$S\$E	-----	-----	-----	-----	-----	-----	-----	-----	-----
chicken	EE\$W\$T\$P\$N\$F\$K\$Q\$C\$W\$N\$S\$1\$NY\$G\$D\$LG\$K\$IA\$E\$C\$T\$F\$K\$M\$R\$S\$N\$S\$A\$R\$V\$L\$F\$S\$G\$S\$L\$R\$K\$C\$R\$S\$A\$C\$C\$Q\$W\$Y\$F\$T\$F\$N\$G\$A\$E\$C\$A\$G\$E\$L\$P\$V\$E\$S\$T\$Y\$T\$D\$Q\$G\$S\$P\$E\$M\$N\$S\$T\$T\$N\$H\$R\$T\$S\$S\$E	-----	-----	-----	-----	-----	-----	-----	-----	-----
in sensus	EE\$W\$T\$P\$N\$%\$K\$Q\$C\$W\$S\$S\$1\$NY\$G\$D\$LG\$K\$IA\$#C\$T\$F\$K\$N\$R\$#S\$A\$R\$V\$L\$F\$S\$G\$S\$L\$R\$K\$C\$R\$#A\$C\$C\$Q\$W\$Y\$F\$T\$F\$N\$G\$A\$E\$C\$A\$G\$E\$L\$P\$V\$E\$S\$T\$Y\$T\$D\$Q\$G\$S\$P\$E\$M\$N\$S\$T\$T\$N\$H\$R\$T\$S\$S\$E	-----	-----	-----	-----	-----	-----	-----	-----	-----
201	210	220	230	240	245	-----	-----	-----	-----	-----
1	1	1	1	1	1	-----	-----	-----	-----	-----
human	GLCEGI\$GAG\$LV\$D\$V\$A\$IW\$G\$T\$C\$D\$P\$K\$G\$D\$A\$S\$T\$G\$W\$N\$S\$V\$R\$1\$1\$E\$E\$LP\$K	-----	-----	-----	-----	-----	-----	-----	-----	-----
mouse	GLCEGI\$GAG\$LV\$D\$V\$A\$IW\$G\$T\$C\$D\$P\$K\$G\$D\$A\$S\$T\$G\$W\$N\$S\$V\$R\$1\$1\$E\$E\$LP\$K	-----	-----	-----	-----	-----	-----	-----	-----	-----
rice_fish	GLCEGI\$K\$A\$G\$LV\$D\$V\$A\$IW\$G\$T\$C\$D\$Y\$P\$R\$G\$D\$A\$S\$T\$G\$W\$N\$S\$V\$R\$1\$1\$E\$E\$LP\$K	-----	-----	-----	-----	-----	-----	-----	-----	-----
zebra_fish	GLCEGI\$H\$A\$G\$LV\$D\$V\$G\$IW\$G\$T\$C\$D\$Y\$P\$R\$G\$D\$A\$S\$T\$G\$W\$N\$S\$V\$R\$1\$1\$E\$E\$LP\$K	-----	-----	-----	-----	-----	-----	-----	-----	-----
chicken	GLCEGI\$A\$G\$LV\$D\$V\$A\$IW\$G\$T\$C\$D\$Y\$P\$R\$G\$D\$A\$S\$T\$G\$W\$N\$S\$V\$R\$1\$1\$E\$E\$LP\$K	-----	-----	-----	-----	-----	-----	-----	-----	-----
in sensus	GLCEGI\$A\$G\$LV\$D\$V\$A\$IW\$G\$T\$C\$D\$Y\$P\$R\$G\$D\$A\$S\$T\$G\$W\$N\$S\$V\$R\$1\$1\$E\$E\$LP\$K	-----	-----	-----	-----	-----	-----	-----	-----	-----

MRPQGPAA\$PQRRLGI\$LLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPGROGSPGANGIPGTPGIPGRDGFKGEKGECLRESF

MCLQGPAGVPG\$RDG\$SP\$GANGIPGTPGIPGRDGFKGEKGECLRESF

110 120 130 140 150

KQCS\$SS\$LN\$Y\$G\$D\$LG\$K\$IA\$E\$C\$T\$F\$K\$M\$R\$S\$N\$S\$A\$R\$V\$L\$F\$S\$G\$S\$L\$R\$K\$C\$R\$N\$A\$C\$C\$Q\$W\$Y\$F

50 170 180 190 200 210

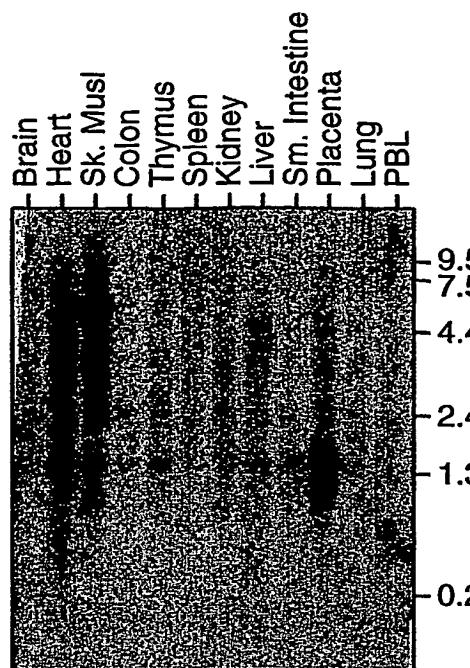
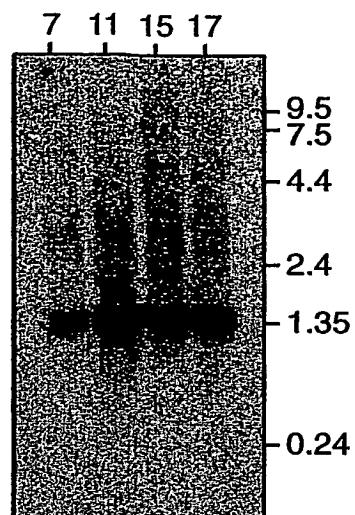
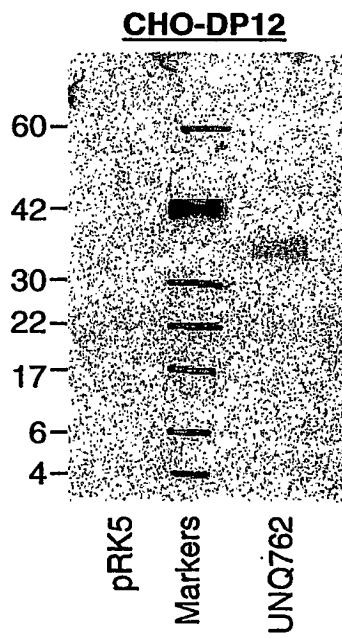
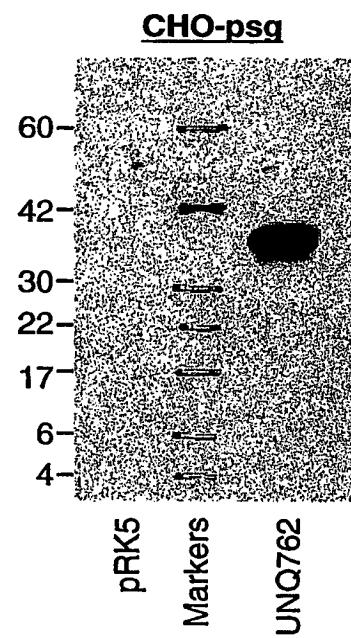
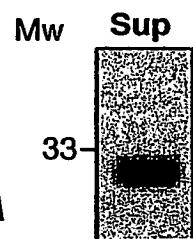
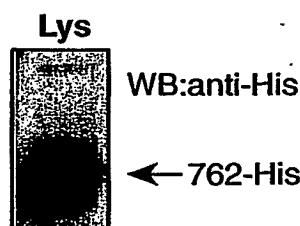
TF\$N\$G\$A\$E\$C\$G\$P\$L\$P\$E\$A\$T\$Y\$T\$D\$Q\$G\$S\$P\$E\$M\$N\$S\$T\$T\$N\$H\$R\$T\$S\$S\$E

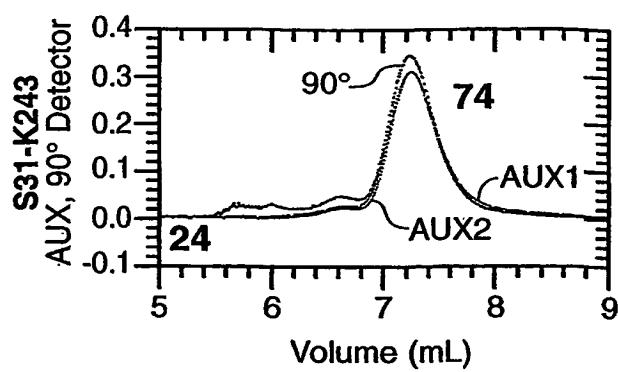
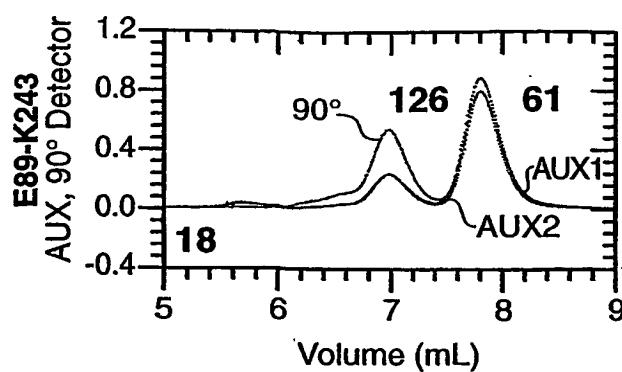
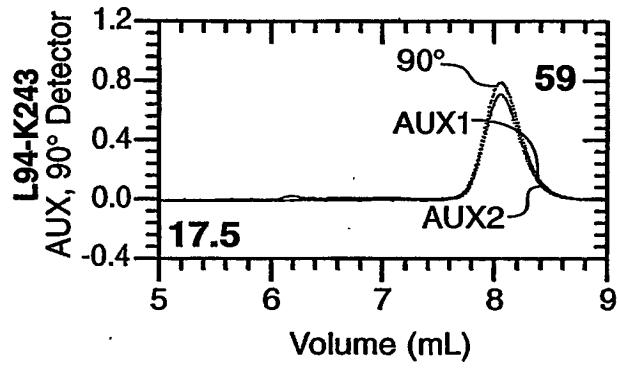
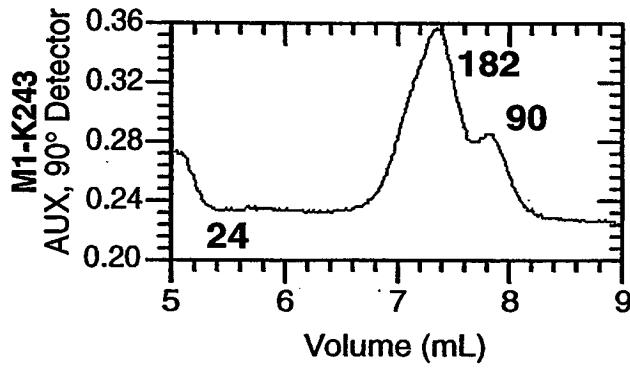
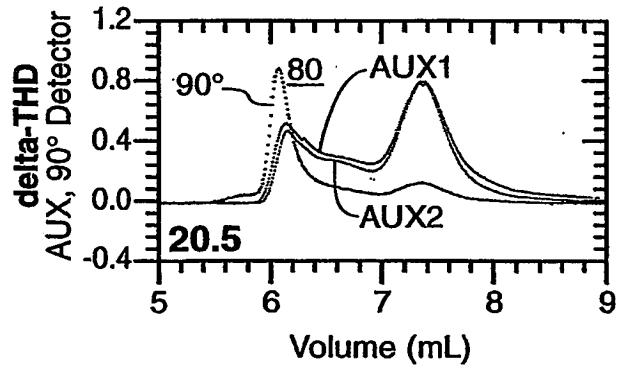
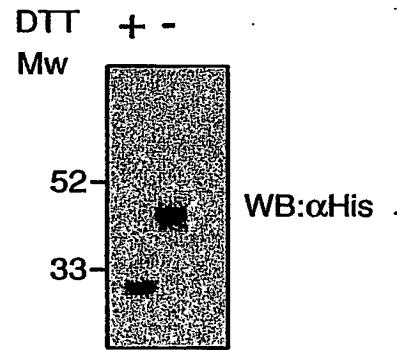
220 230 240

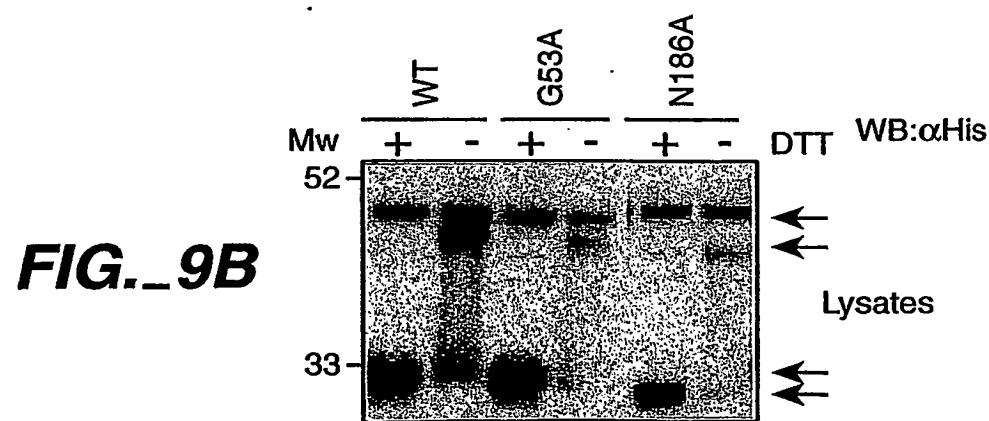
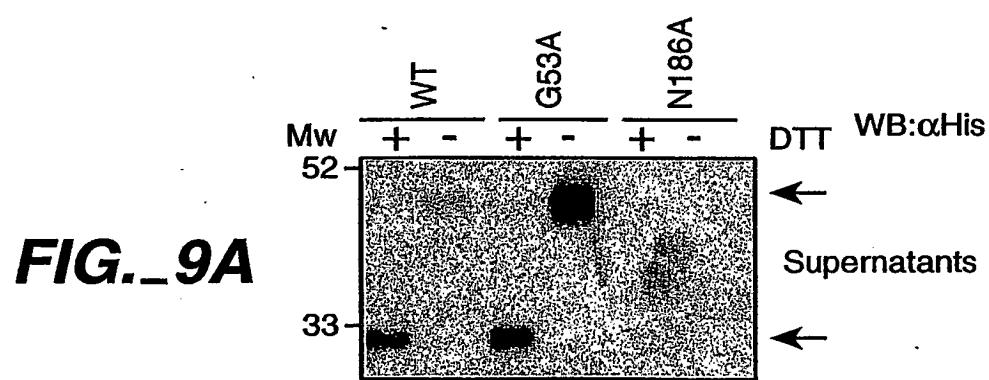
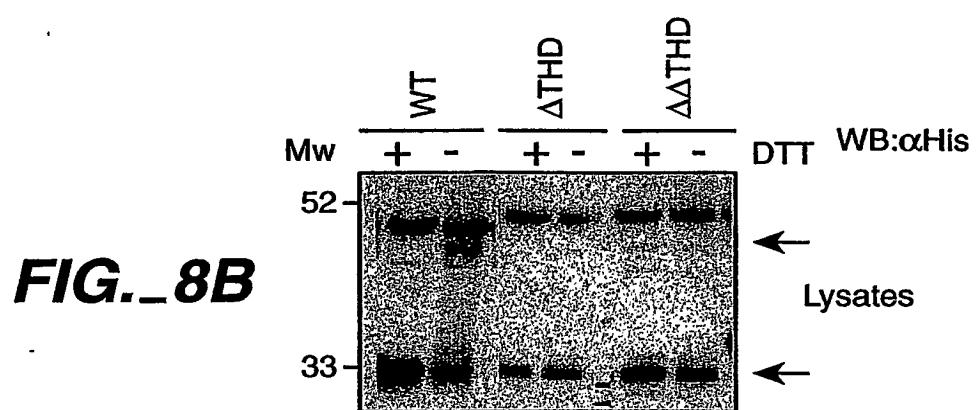
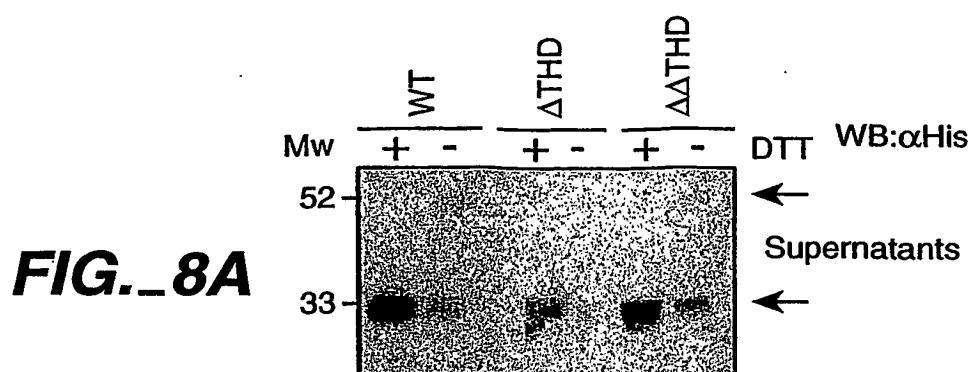
IW\$G\$T\$C\$D\$Y\$P\$K\$G\$D\$A\$S\$T\$G\$W\$N\$S\$V\$R\$1\$1\$E\$E\$LP\$K

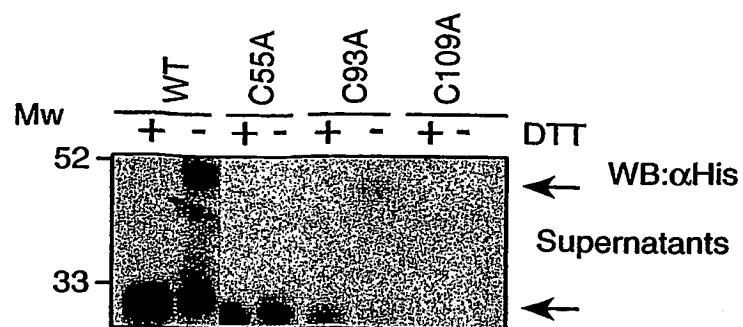
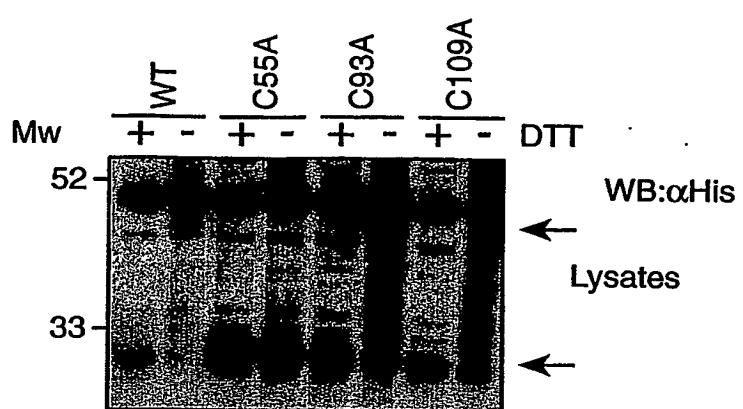
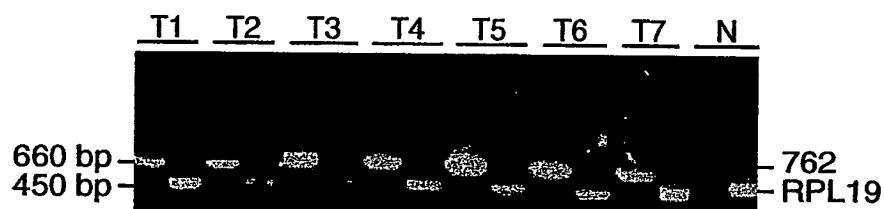
**FIG. - 1**

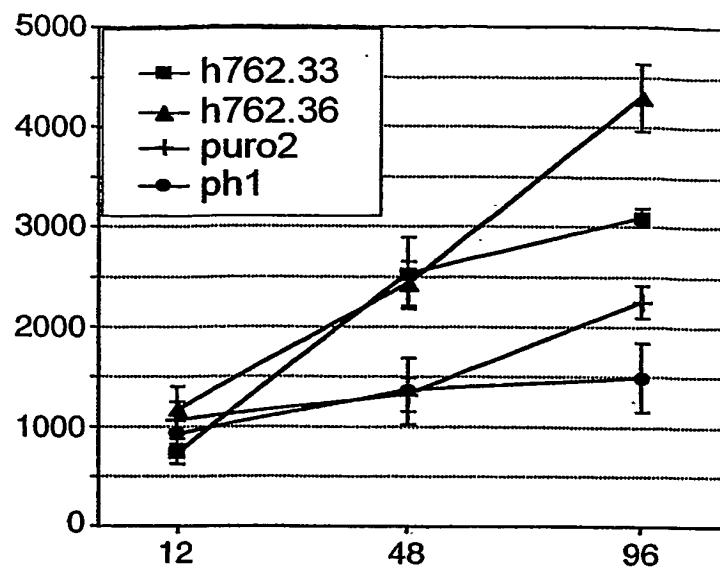
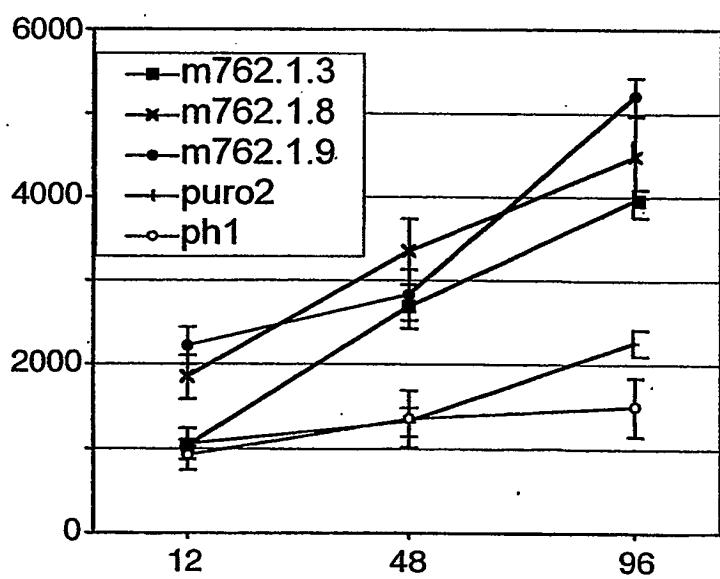
**FIG. - 2**

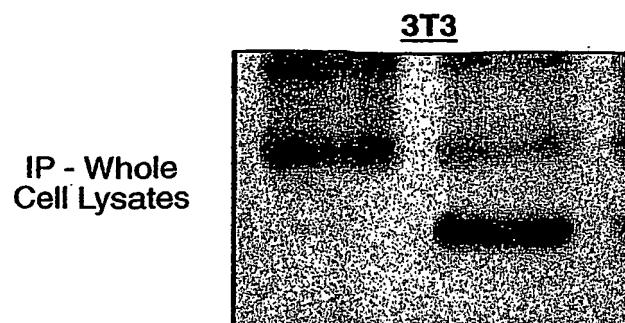
**FIG.\_3A****Embryonic Days****FIG.\_3B****FIG.\_4A****FIG.\_4B****FIG.\_5A****FIG.\_5B**

**FIG.\_6A****FIG.\_6B****FIG.\_6C****FIG.\_7A****FIG.\_7B****FIG.\_7C**

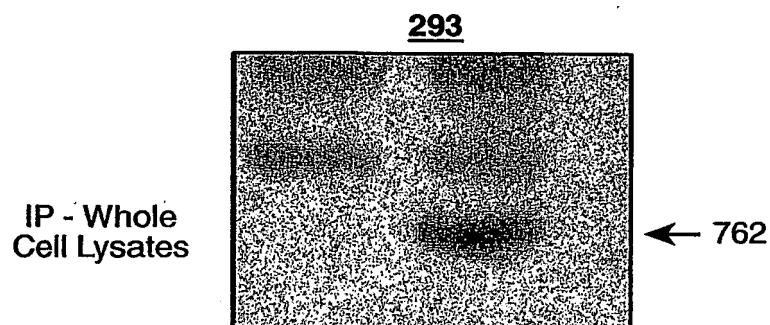


**FIG.\_ 10A****FIG.\_ 10B****FIG.\_ 11**

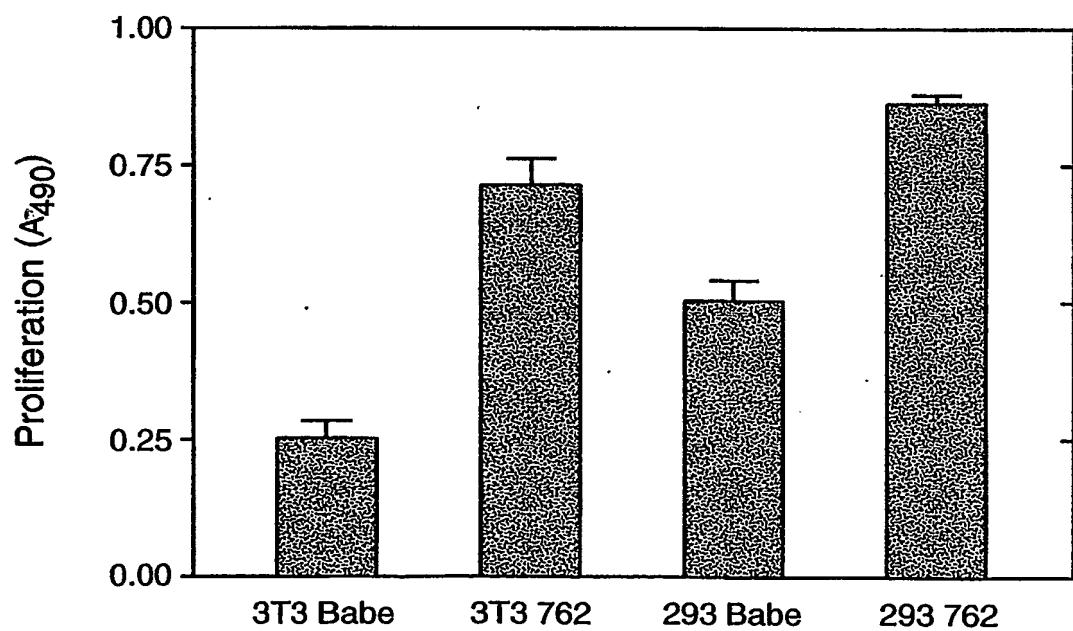
**FIG. 12A****FIG. 12B**



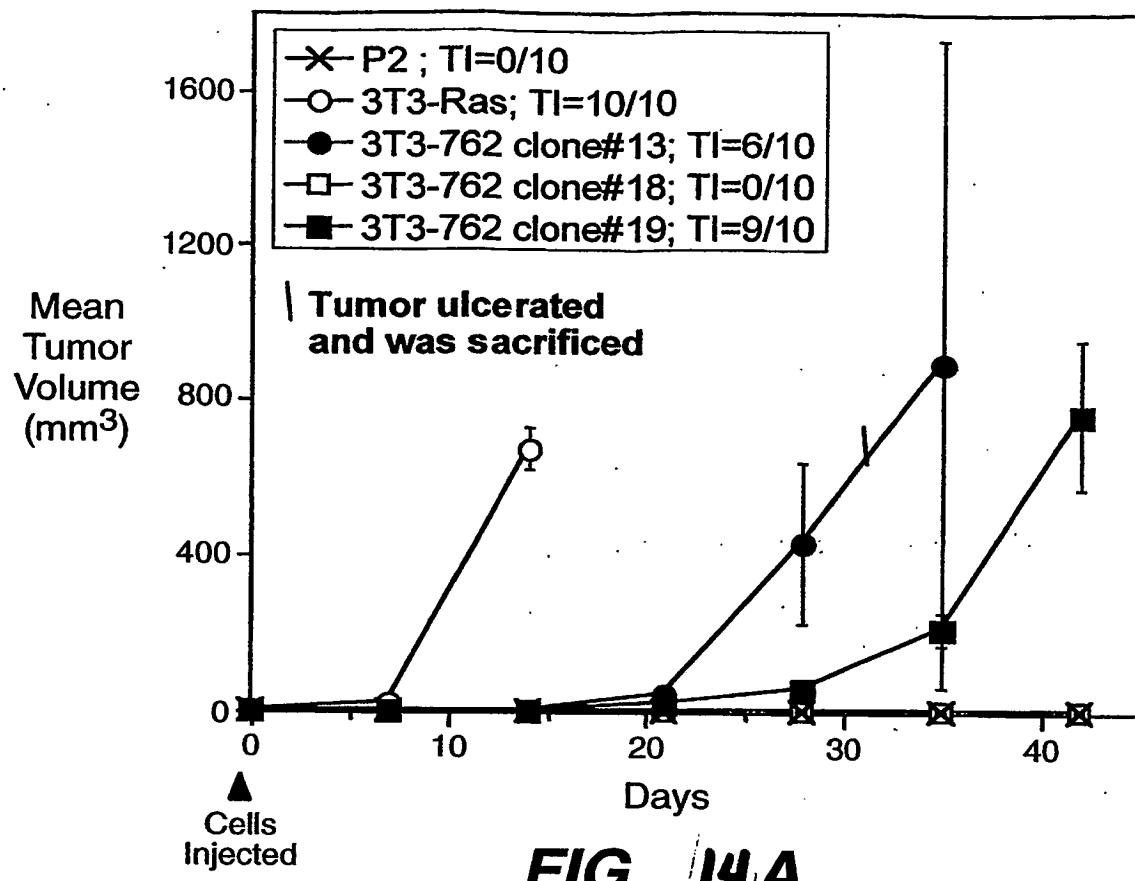
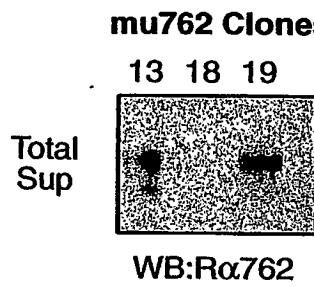
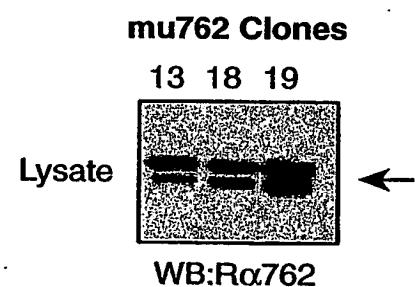
**FIG. 13.A**

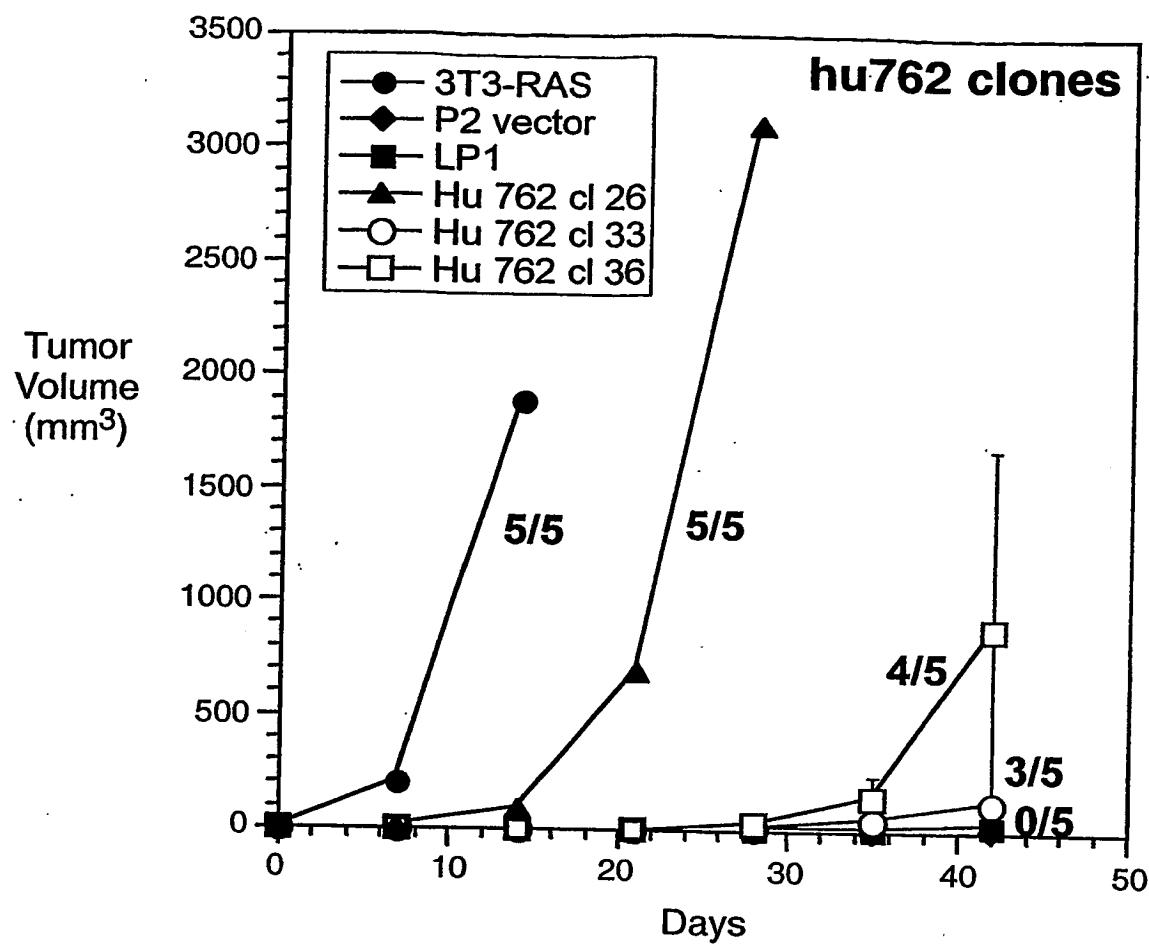


**FIG. 13.B**

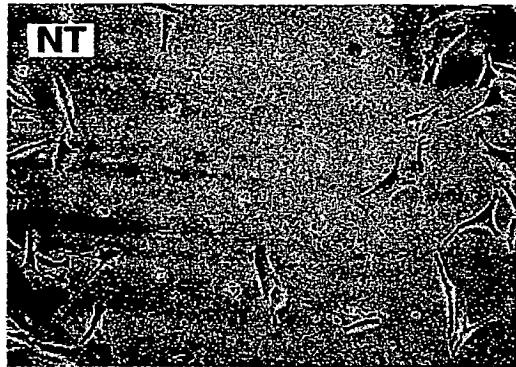
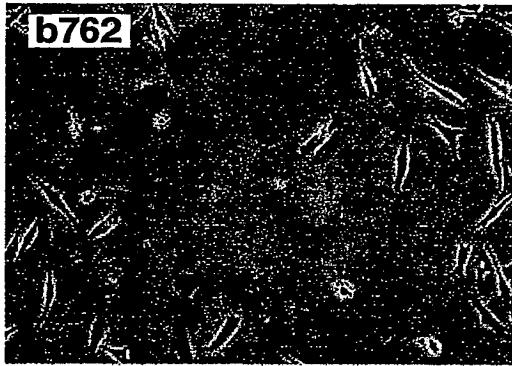
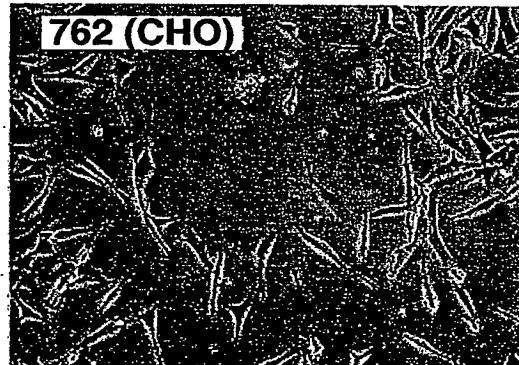


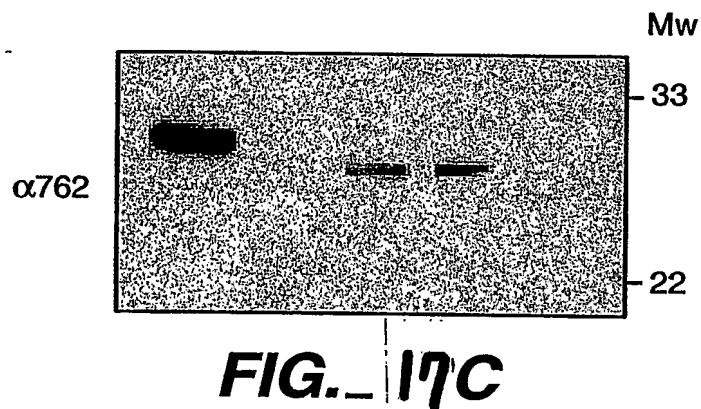
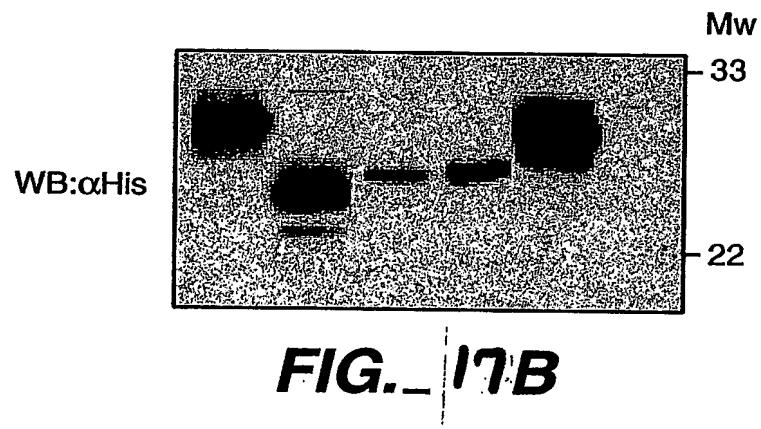
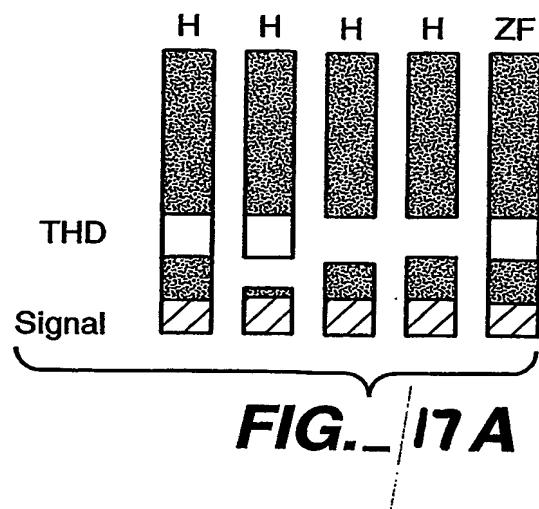
**FIG. 13.C**

**FIG. 14A****FIG. 14B****FIG. 14C**



**FIG. 15**

**FIG. 16 A****FIG. 16 C****FIG. 16 B****FIG. 16 D****FIG. 16 E**



H1			H2			H3			H3																						
8	29	30	31	32	33	49	50	51	52	52a	53	54	55	56	57	58	92	93	94	95	96	97	98	99	100	100a	100b	100c	101	102	Name
-	S	G	S	D	G	R	I	S	P	Y	G	G	N	T	N	C	A	R	V	G	G	L	K	L	-	F	D	Y	S7		
-	T	N	S	D	A	T	I	Y	P	Y	G	G	G	G	G	G	C	A	R	G	G	M	D	G	Y	V	M	D	Y	S16	
-	N	N	Y	D	G	Y	I	S	P	P	G	S	G	A	T	Y	C	A	R	M	V	G	M	R	R	G	V	M	D	Y	F5
-	N	N	Y	D	G	Y	I	S	P	P	G	S	G	A	T	Y	C	A	R	M	V	G	M	R	R	G	V	M	D	Y	F6
-	S	G	S	W	A	W	I	A	P	Y	S	G	A	T	D	C	A	R	E	G	G	L	Y	W	V	-	F	D	Y	S4	
-	S	N	Y	G	G	R	I	S	P	S	N	G	S	T	Y	C	A	K	C	S	V	R	-	-	-	-	F	A	Y	S9	
-	S	G	S	W	A	W	I	A	P	Y	S	G	A	T	D	C	A	R	E	G	G	L	Y	W	V	-	F	D	Y	F13	
-	S	G	S	W	A	W	I	A	P	Y	S	G	A	T	D	C	A	R	E	G	G	L	Y	W	V	-	F	D	Y	F47	

FIG.- 18

Phage	Fab			IgG		
	762 S/S	762 F/F	762 S/S	762 F/F	762 S/S	762 F/F
S4	3nM	0.9nM	3.6nM (1.9nM)	32nM	13.4nM	0.5nM
762 S/S	762 F/F	762 S/S	762 F/F	762 S/S	762 F/F	3.1nM
S7	35nM	2.7nM	113nM	57nM	n/a	7.3nM
						41nM

FIG.- 24

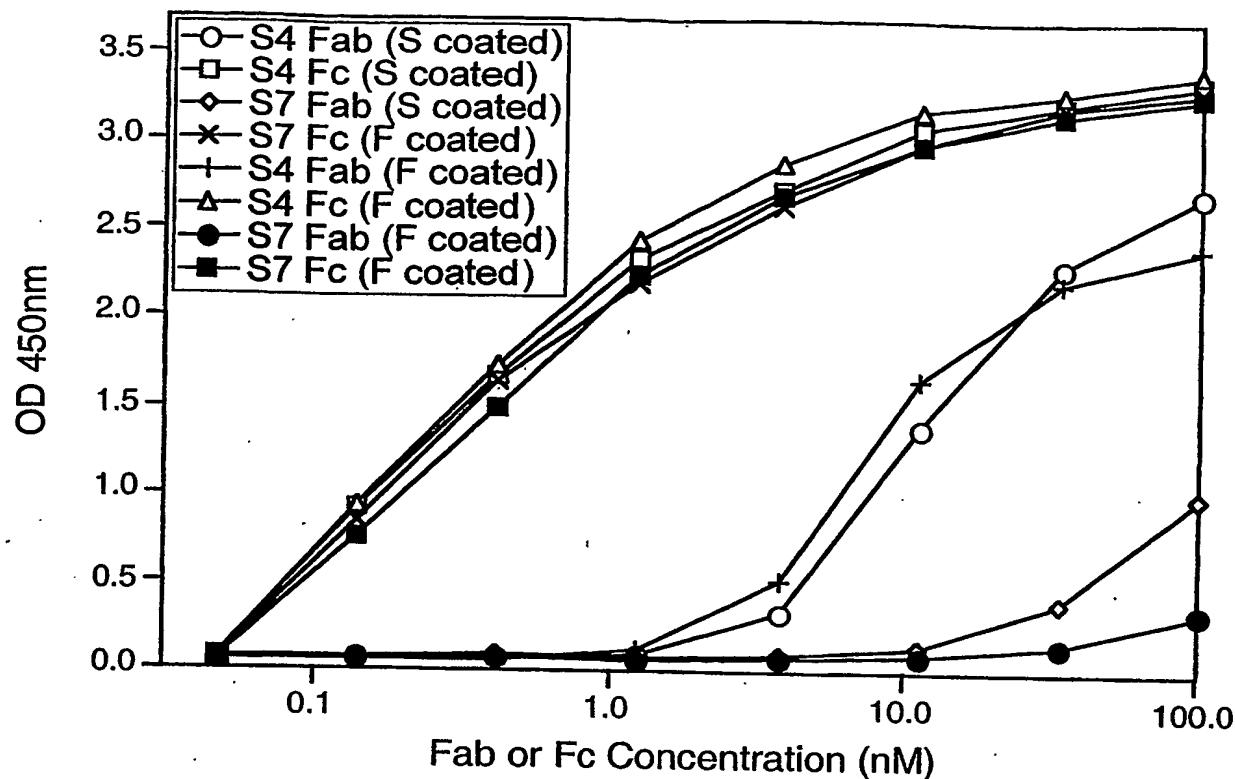
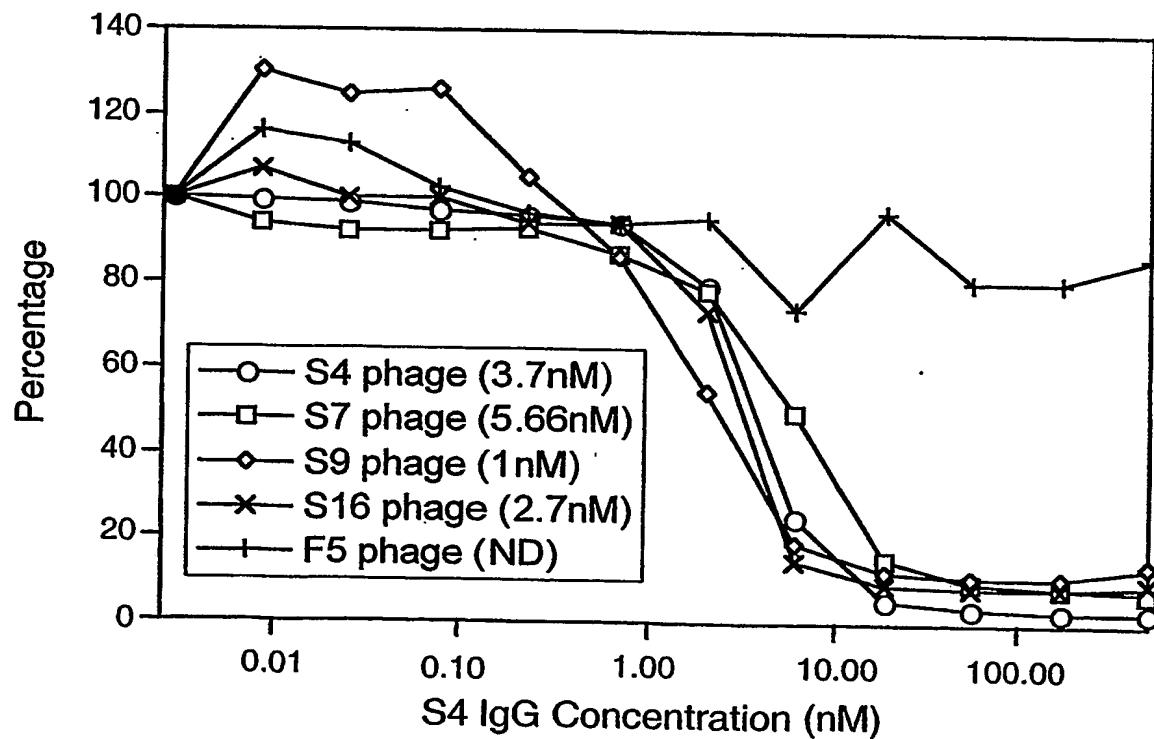
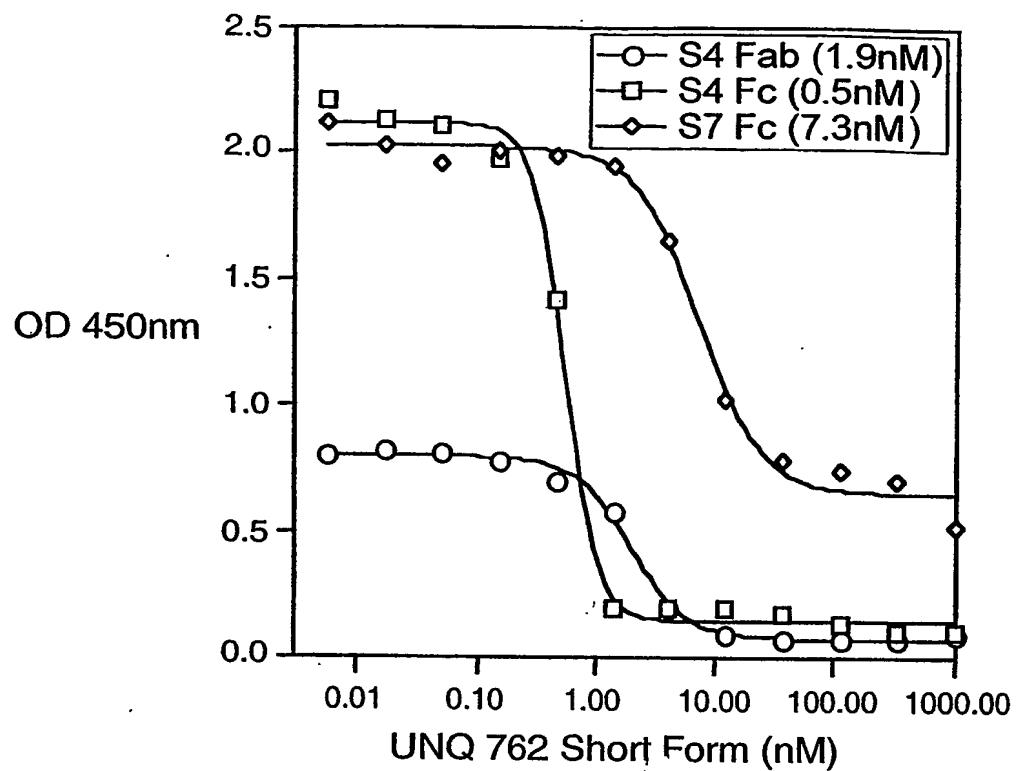
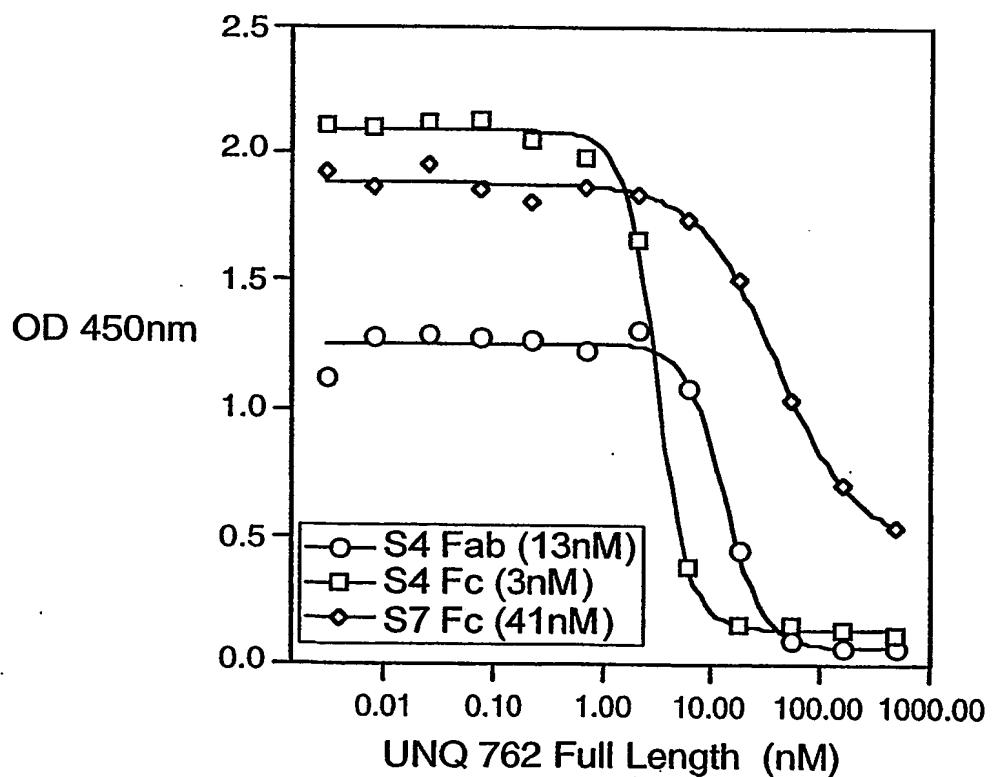


FIG. 19

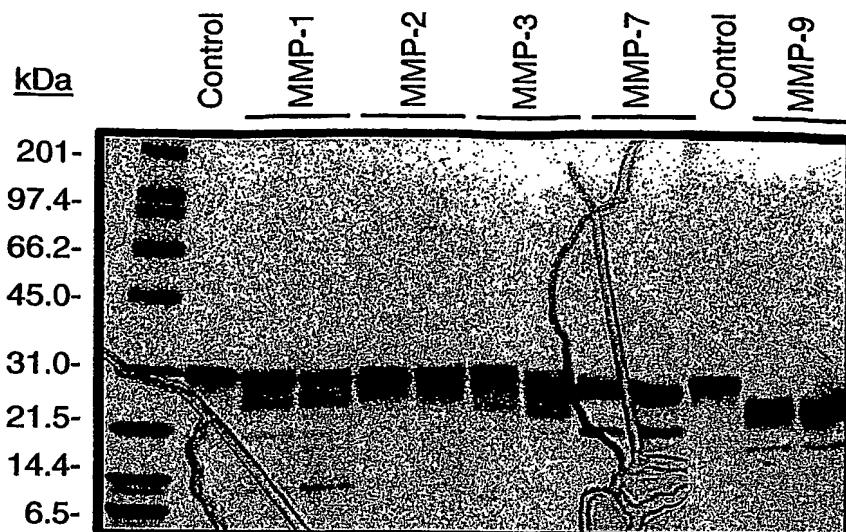
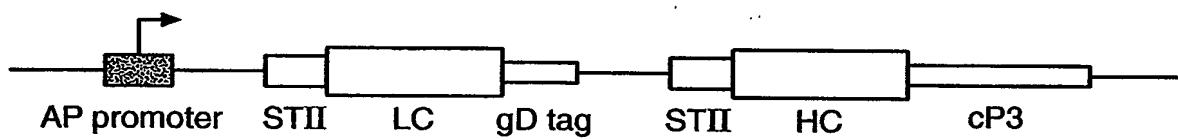
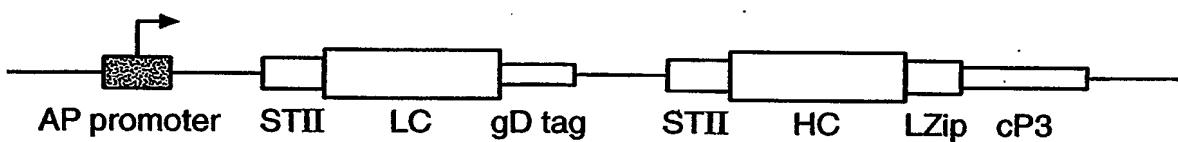
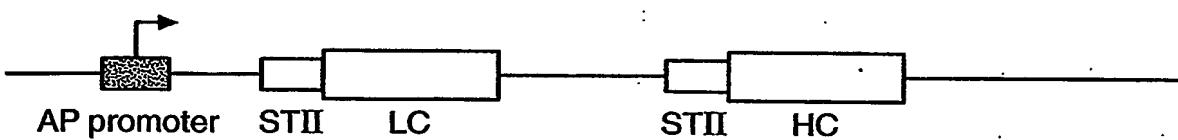
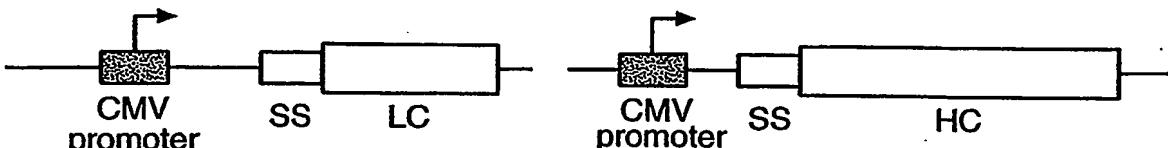
FIG. 27  
13/75



**FIG. 20A**



**FIG. 20B**

**FIG. 23****FIG. 24 A****FIG. 24 B****FIG. 24 C****FIG. 24 D**

1 GAATTCAACT TCTCCATACT TTGGATAAGG AAAACAGAC ATGAAALATC TCATTCGTGA GTTGTATT AAGCTTGCCC AAAAGAAA AGAGTCGAAT  
 CTTAAGTTGA AGGGTATGA AACCTATCC TTATGTCG TACTTTAG AGTAAAGACT CAACAAATAA TTCGAACGGG TTTTCTCTCTCTCTCTA  
 101 GAACTGTG CGCAGGTAGA AGCTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGG GTTGATGGAT CAGGTAGAGG  
 CTTGACACAC GCCTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTAAC CGCGTTTAC CGCTGTGCG CAACTAACTA GTCCATCTCC  
 201 GGGGGTGTAA CGAGGAAAG CCCGATGCCA GCATTCCTGA CGACGATACG GAGCTGTGC CGACGATACG GAGCTGTACG CGCTAATGCA TTGTAAGCTA CTCGTCAGTA  
 CCCGGACAT GCCTCCATTTC GGGCTATCGGT CGTAAAGGACT GCTGCTATGC CTGACCGACG CGCTAATGCA TTGTAAGCTA CTCGTCAGTA  
 301 AAAAGTAAAT CTTTCAACA GCTGTCAAA AGTGTCAAG GCGGAGACTT ATAGTCGCTT TGTTTTATT TTGTAATGTA TTGTAACTA GTACGCAAGT  
 TTGTCATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTGTCAA TATCAGCGAA ACAAAATAA AAAATTACAT AACATTTGAT CATGCGTTCA  
 401 TCACGTAAA AGGGTATGTA GAGGTGAGG TGATTTATG AAAAGATA TCGCAATTCT TCTTCATCT ATGTCGATCT ATGTCGTTT TTCTATGTC TACAATGCC  
 AGTGCATTTC TCCCATACAT CTCCAACTCC ACTAAATAC TTGTTCTAT AGCGTAAGA AGAACGTAGA TACIAGAAA AAAGATAACG ATGTTACGG  
 1 M K K N I A F L L A S M F V F S I A T N A  
 ^ start of stII signal sequence  
 ^met

501 TATGGAGATA TCCAGATGAC CCAGTCCCCG AGCTCCCTGT CCGCCCTGT GGGGATAGG GTCACCATCA CCTGCGTGC CAGTCAGGAT GTGTCACACTG  
 ATACGTCTAT AGGTCTACTG GGTCAAGGGGC TCGAGGGACA GGGGGAGACA CCCGCTATCC CAGTGGTAGT GGACGGCAGC GTCAAGTCTTA CACAGGTGAC  
 22 Y A D I Q M T Q S P S S L S A S V G D R V T I T C R A S Q D V S T A  
 ^ start of light chain

601 CTGTAGCCTG GTATCAACAG AAACAGGAA AAGCTCCGAA GCTTCTGATT TACCTGGCAT CCTCCCTCTA CTCTGGACTC CCTTCTCGCT TCTCTGGTAG  
 GACATGGAC CATAGTGTCTT TTGGTCTT TTGAGGCTT CGAAGACTAA ATGAGCCGTA GGAAGGAGAT GAGACTCTAG GGAAAGGGCA AGAGACATC  
 56 V A W Y Q K P G K A P K L L I Y S A S F L Y S G V P S R F S G S  
 ^ start of light chain

701 CGGTTCGGGG ACGGATTCA CTCGTACCAT CAGGAGTCTG CAGCCGGAG ACTTCGCAAC TTATTACTG CAGCAATCTT ATACTACTCC TCCCACTTC  
 GCCAAGGGCCC TGCCTAAAGT GAGACTGGTA GTGGTCAGAC GTGGCCTTC TGAAAGCTTG ATAATGACA GTCAAGTGGAGG AGGGTGCAG  
 89 G S G T D F T L T I S S L Q P E D F A T Y Y C Q Q S Y T T P P T F  
 ^ start of light chain

FIG.- 25A

301 GGACGGTA CCAAGGGAA GATCAAACGA ACTGTGGCTG CACCATCTGT CTTCATCTTC CGGCCATCTG ATGAGGAGTT GAAATCTGGAA ACTGCCCTCTG  
 122 CCTGTCAT GGTCCACCT CTAGTTTCTG TGACACCCAC GIGGTAGACA GAAGTAGAAG GGGGTAGAC TACTCTGCAA CTTAGACCT TGACGGAGAC  
 301 TTGTGTGCCT GCTGATAAC TTCTATCCCA GAGAGGCCAA AGTACAGTGG AAGGTGGATA AGGCCCTCCA ATCGGTAAC TCCAGGAGA GTGTCAACAGA  
 156 V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E  
 301 GCAAGCACGC AAGGACAGCA CCTACAGCCCT CAGGAGCACC CTGACGGCTGA GCAAGGAGA CTACAGAGAA CACAAAGTCT ACGCCCTGCGA AGTCACCCAT  
 CGTCCCTGTCG TTCCCTGTCG GGATGTCGGA GTCGTGTGG GACTGGCACT CGTTCTGCTT GATGCTCTT GTGTTTCAGA TGAGTGGGTA  
 .89 Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H  
 .01 CAGGGCCCTGA GCTGCCCGT CACAAAGAGC TTCAACAGGG GAGAGTGTGG TGCCAGGCTCC GGTATGGCTG ATCCGAACCG TTTCGGGGT AAGGACCTGG  
 GTCCGGACT CGAGGGGCA GTGTTTCTCG AAGTGTCCC CTCTCACACC ACGGTGGG COATACCGAC TAGGCTGGC AAAGGGCCA TTCCCTGGACC  
 .22 Q G L S S P V T K S F N R G E C G A S S G M A D P N R F R G K D L A  
 ^end of light chain, start of gd tag

17/75 01 CATAACTGCA GGCTGATCCT CTACGCCGA CGCATCTGTG CCTAGTAGC CAAGTCACG TAAAGGGT AACTAGAGGT TGAGGTGATT TTATGAAAAA  
 GTATTGAGCT CCGACTAGGA GATGGGGCCT GCGTAGGCC GGGATCATGC GTCAAGTGC ATTTCATCCA ACTCCACTAA AATACTTTT  
 .56 O  
 .23

M K K  
 ^start of stII

01 GAATATCGCA TTTCTCTTG CATCTATGTT CGTTTCTT ATTGCTACAA ACGCGTACGC TGAGGTTCAAG CTGGTGGAGT CTGGGGTGG CCTGGTGCAG  
 CTTATAGCGT AAAGAGAAC GTAGATACAA GCAAAAGA TAAGGATGTT TGGCATGCG ACTCCAAGTC GACCACCTCA GACCGCCACC GGACCACTCA  
 20 N I A F L L A S M F V F S I A T N A Y A E V Q L V E S G G G L V Q  
 ^start of heavy chain

01 CGAGGGGCT CACTCGTTT GTCCTGTGCA GCTTCGGCT TOAACATTAA AGACACTAT ATACACTGGG TGCCTCAAGG CCGGGTAAG GGCTGGGAT  
 GGTCCCCGAA GTGAGGCAA CAGGACACGT CGAAGACCGA AGTTGTAATT TCTGTGGATA TATGTGACCC ACGGCAGTCCG GGGCCATTG CGGACCTTA  
 14 P G G S L R L S C A A S G F N I K D T Y I H W V R Q A P G K G L E W  
 ^CDR-H1

FIG. - 25 6

1501 GGTTGCAAG GATTATCCT ACGAATGGTT ATACTAGATA TGCCGATAGC GTTCAAGGGCC GTTCAACTAT AAGGGCAGAC ACATCCAAA ACACAGCCTA  
 CCCAACGTTCCCTAAATAGGA TGCTTACCAA TATGATCTAT ACGGCTATCG CAGTTCGGG CAAAGTATA TTCGGGTCTG TGTAGGTTT TGTGTGGAT  
 48 V A R I Y P T N G Y T R Y A D S V K G R F T I S A D T S K N T A Y  
 ^CDR-H2

1601 CCTACAAATG AACAGCTTAA GAGCTGAGGA CACTGCCGTC TATTATGTA GCGCTGGGG AGGGACGGG TCTATGCTA TGACTACTG GGGTCAAGGA  
 1602 GGATGTTAC TTGTCGAATT CTCGACTCCT GTGACGGCAAG ATAATAACAT CGGGGACCCC TCCCCTGCCG AAGATACGAT ACCTGTGAC CCCAGTTCTT  
 81 L Q-M N S I R A. E D T A V Y I C S R W G G D G F Y A M D Y W G Q G ^CDR-H3

11701 ACACTAGTCA CGGTCTCCCTC GGCTTCCACC AGGGCCAT CGGTCTCCCTC CGGTCTCCCTC

114 T L V T V S S A S T K G P S V F P L A P S S K S T S G G T A A V G C

11801 GCCTGGTCAA GGAAGTCTTC CCCGAACCGG TGACGGTGTG CCGGGCTGTA CCAGGCCCTTC GCACACCTTC CCGGGCTGTCC · TACAGTCCCT

1875

2001 GTCGACAAGA AAGTTGAGCC CAAATCTTGT GACAAAACCT ACCTCAGTGG CGGTGGCTCT GGTTCCGGTG ATTTCGATTA TGAAAAGATG GCAAACGGCTA  
CAGCTGTTCT TTCAACTCGG GTTTAGAACCA CTGTTAGAACCA TGAGACTCACC GGACCCGAGA CAAAGGCAC TAAACTAAT ACTTTTCTAC CGTTGCGAT  
214 V D K K V E P K S C D K T H L S G G S G S G D F D Y E K M A N A N

^start of gene III coat protein (267-end)  
32 heavy chain

2101 ATAAGGGGGC TATGACCGAA AATGCCGATG AAAACGCGCT AACTTGACTGAC GCTAAAGGCA AACTTGCTACT GATTACGGTGTCTGCTATCGA  
TATTCCCCCG ATACTGGCTT TTACGGCTAC TTGTCAGACTG CGATTTCGGT TTGAACTAAG ACAGGGATGA CTAATGCCAC GACGATAGCT  
248 K G A M T E N A D E N A L Q S D A K G K L D S V A T D Y G A A I D

FIG. 25 C

2201 TGGTTTCATT GGTGACGGTT CGGGCTTGC TAATGGTAAT GGTGGCTACTG GTGATTTCGC TGGCTCTAAT TCCCAAATGG CTCAAAGTGG TGACGGTGG  
 ACCAAAGTAA CCACTGCAA GCGCGAACG ATTACCATTA CCACGATGAC CACTAAAAG ACCGAGATTAA AGGGTTTACCGTTAGGACTAGCC ACTGCCACTA  
 281 G F I G D V S G L A N G N G A T G D F A G S N S Q M A Q V G D G D  
  
 2301 AATTACCTT TAATGAATAA TTTCGTCAA TATTTACCTT CCCTCCTCA ATCGGGTGA TGTCGCCCTT TTGTCCTTAG CGCTGGTAA CCATATGAAT  
 TAAAGTGGAA ATTACCTTT AAAGGCAGTT ATAATGGAA GGGAGGGAGT TAGGCCAACTT ACAGGGGAA AACAGAAATC GCGACCATT GGTTATCTTA  
 314 N S P L M N N F R Q Y L P S L P Q S V E C R P F V F S A G K P V E F  
  
 2401 TTTCTATTGA TTGTGACAAA ATAAACTTAT TCGGGGTGT CTTTGCCTT CTTTTATATG TTGCCACCTT TAATGTATGTA TTTTCTAGT TTGCTAACAT  
 AAAGATAACT AACACTGTGT TATTTGAATA AGGCACCACA GAAACGCAA AACGAAATAC AACGGGGAA ATTCATACAT AAAAGATGCA AACGATGTA  
 348 S I D C D K I N L F R G V F A F L L Y V A T F M Y V F S T F A N I  
  
 2501 ACTGGCTTAAT AGGGACTT AATCATGCCA GTTCTTTGG CTAGGGCCGC CCTATACCTT GTCTGCCCTCC CCGGGTGGCA TGGAGCCGG  
 TGACGCCATTAA TCCCTCAGAA TTAGTACGGT CAAGAAAACC GATCGGGGG GGATATGAA CAGACGGGG GGGCAACGC AGGCCAACGT ACCTGGCCC  
 381 L R N K E S O  
  
 2601 CCACCTCGAC CTGAATGGAA GCCAAAGGCA CCTCGCTAAC GGATTOACCA CTCCAAGAAT TGGAGCCAT CAATTCTTGC GGAGAACTGT GAATGGCAA  
 GGTGGAGCTG GACTTACCTT CGGGCGCGT GGAGCGATTG CCTAAGGGT GAGGTCTTA ACCTCGGTTA GTTAAGAACG CCTCTTGACA CTTACCGGTT  
  
 2701 ACCAACCCCTT GGCAGAACAT ATCCATCGCG TCGGCCATCT CCAGGAGCCG CACGGGGCGC ATCTCGGCCA GCGTTGGTC CTGGCCACGG GTGGCGCATGA  
 TGGTTGGAA CGCGAACTC TAGGTAGCA AGGGGTAGA GGTCTGGC GTGCGCCGG TAGAGCCGT CGCAACCCAG GACCGGTGCC CACGGGTACT  
  
 2801 TCGTGGCTCTT GTCGTTGAGG ACCCGGCTAG GCTGGGGGG TTGCTACTG GTTAGCCAGA ATGAATCACC GATACGCCAG CGAACGTGAA GCGACTGCTG  
 AGCACGAGGA CAGCAACTC TGGCCGATC CGACCGGGCC AACGGAAATGA CCAATCGTCT TACTTAGGG CTATGGCTC GCTTGCACCT CGCTGACGAC  
  
 2901 CTGCAAAACG TCTGGACCT GAGCAACAAAC ATGAATGGTC TTCGGTTTCGTA AAGTCTGGAA ACGGGAAGT OAGGGCCCTG CACCATTTG  
 GACGGTTTGC AGACGCTGGA CTCGTTGTTG TACTTACCGA AAGCCAAAGCAT TTCAAGACCTT TGGCCCTTCA GTCGGGGGAC GTGGTAATAC  
  
 3001 TCCGGATCT GGTGGCAGG ATGCTGCTGG CTACCCCTGTG TACCTACCGA AACACCTAC ATCTGTATTA ACGAAGGGCT GGCATGTGACC CTGAGGTATT TTTCTCTGGT  
 AAGGCCTAGA CGTAGGGTCC TACGACGACC GATGGGACAC CCGTAACTGG TAGACATAAT TGCTTGGATG AAAGAGACCA

101 CCCGCCAT CCATACCGCC AGTGTGTAC CCTCACAAAC TICCACTAAC CGGGCATGTT CATCATAGT ACCCGTATC GTGAGCATCC TCTCTCGTT  
 201 GGGGGCGTA GGTATGGGG TCAACAAATG GGAGTGTGC AAGGTCAATG GCCCGTATG AGGTACAGA TTGGGCATCA TTGAGTAGG CACTCGTAGG AGAGAGCAA  
 301 CATGGTATC ATTACCCCA TGAACAGAAA TTCCCCCTTA CACGGGGCA TCAAGTGACC AACAGGAA AACCGCCCT TAACATGGCC CGCTTATCA  
 GTAGCCATAG TAATGGGGT ACTTGTCTT AAGGGGAAT GTGCTCCGT AGTTACTGG TTGTCCTT TTGGGGGA ATGTACCGG GCGAAATAGT  
 301 GAAGCCGAC ATTAAACGTT CTGGAGAAC TCAACGGACT GGACGGGAG AACAGGGAG ACATCTGTAA ATCGCTTCAC GACCACGCTG ATGAGCTTA  
 CTTGGTCTG TAATGGCGAA GACCTCTTGT AGTGTCTCGA CCTGGCCCTA CTGGTCCGT TGTAGACACT TAGCGAAGTG CTGGTGCAC TACTCGAAAT  
 401 CGGCAGGATC CGGGAAATTGT AAAAGTTAAATTTGTAA AATTTCGGTT AAATTGTAAATTTGT TAATAGCT CATTTTAA CCAATAGGCC GAAATCGGCA  
 GGCCTCTAG GCCTTAACA TTAGGGCAA TAAACAAATT TTAAACAACTT CTCACAAACAA GTTAAACAA ATTAGTCGA GTAAAAATT GTTATCCGG CTTTAGCCGT  
 501 AAATCCCTTA TAAATCAAA GAATAGACCC AGATAGGGT GAGTGTGTT CCAGTTGGA ACAAGAGTC ACTATTAAAG AACGTGGACT CAAACGTCAA  
 TTTAGGGAAATTAGTTT CTATCTGGC TCTATCCCA CCTAACAAACAA GTTAAACAACT TGTCTCAGG TGATAAATTTC TTGACCTGA GGTACCTGA  
 601 AGGGCGAAA ACCGCTATC AGGGCTATGG CCCACTACGTA GTAACCATCAC CCTAACATCAAG TTTTTGGG TCAGGGTGGCC GTAAAGGACT AAATCGAAC  
 TCCCGCTTT TGGCAGATAG TCCCGATACC GGGTGTAGCA CTGGTGTAGTG GGATTAGTTC AAAAACCCC AGCTCCACGG CATTTCGTGA TTAGCCCTG  
 701 CCTAAAGGGAA GCCCCGATT TAGAGCTTGA CGGGAAAGC CGGGAACGT GGGGAAAG GAAAGGAAGA AAGCAGAAAG AGCGGGGGCT AGGGCGCTGG  
 GGATTCCCT CGGGGCTAA ATCTGAACCT GCCCCTTTCG GCGCTTGCAC CCCTCTTTC CTCTCCCTCT TTGCTTTCC TCGCTTCC TCGCTTCC  
 801 CAAGTGTGG CGTACCGCTG CGCGTAACCA CCACACCCCG CGCGCTTAAAT GCGCCGTAC AGGGCGCTC CGGATCTGC CTGGTGTAGA  
 GTTCACATCG CGCGCATCG GCGCATTTGT GGTGTGGGG CGCGGAATTA CGCGGTGATG TCCCGGGCAG GCCTAGGACG GAGGGGCAA AGCCACTACT  
 901 CGGTGAAAC CTCTGACACA TGCAGCTCCC GGAGACGGTC ACAGCTTGTIC TGTAAAGGGA TGCCTGGGAGC AGACAAAGCCC GTCAGGGGG  
 GCCACTTTG GAGACTGTGT ACGTGGGG CCTCTGCCAG TGTGAAACAG ACATTGGCT ACGGCCCTCG TCTGTTGGG CAGTCGCCA CAGTCGCCA  
 101 GTGGGGGT GTGGGGGG AGCCATGACC CAGTOACGTA GGGATAGGG AGGTATAACT GGTTAACTA TGCGGGCATCA GAGCAGATT TACTGAGGT  
 CAACCCCA CAGCCCCGGC TCGGTACTGG GTCAGTGCAT CGCTATGCC TCACATATGA CGGAATTGAT ACGGCCTAGT CTGCTTAAC ATGACTCTCA

4101 GCACCATATG CGGTGTGAAA TACCGCACAG ATGGTAAGG AGAAAATACC GCATCAGGGG CTCTTCCGCT TCCCTCGCTA CTGACTCGCT GCGCTCGGTC  
CGTGGTATA GCACACTTT ATGGCGTGTCA TAGCATTCC TCTTATGG CGTACTCGGC GAGAAGGGGA AGGAGGAGT GACTGAGGA CGCGAGGCCAG

4201 GTTCGGCTGC GGCGAGGGGT ATCAGCTCAC TCAAAGGGGG TAATACGGTT ATCACAGAA TCAGGGGATA ACGGAGGGAA GAACATGTGA GCAAAAGGCC  
CAAGCCGACG CGCGTCGCCA TAGTCAGGTG AGTTCAGGT ATTATGCCAA TAGTGCCTT AGTCCCTAT TGCGTCTT CTGTACACT CGTTTCCGG

4301 AGCAAAGGC CAGGAACCGT AAAAGGGCG CGTGGCTGGC GTTTTCCAT AGGCTCCGCC CCCCTGACGA GCATCACAA AATCGACGCT CAAGTCAGAG  
TCGTTTCCG GTCCCTGGCA TTTTCCGGC GAAACGACCG CAAAGGTA TCCGAGGGG GGGGACTGCT CGTACGTCTT TAGCTGCCA GTTCAGTCTC

4401 GTGGCGAAC COGACAGGAC TATAAAGATA CCAGGGGTTT CCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC TGGATACCTG  
CACCGCTTTCG GGCTGTCTC ATATTCTAT GGTCCGGAAA GGGGACCTT CGAGGGAGCA CGCGAGAGGA CAAGGCTGGG ACGGGAATG GCCTATGGAC  
AGGGGGAAAG AGGGAAAGCCC TTGCAACGCG GAAAGAGTAT CGAGTGGAC ATCCATAGAG TCAAGCCACA TCCAGCAAGC GAGGTTCGAC CGGACACAGC

4501 TCCGGCTTTC TCCTCTGGG AAGCTGGCG CCTTCTCATCA GCTCACGGCTG TAGGTATCTC AGTCGGTT AGGTGTTG CTCCAAGGCTG GGCTGTGTC  
TGCTTGGGG GCAAGTGGG CTGGCACCGC GGAATAGGCC ATTGATAGCA GAACTCAGGT TGTGCTGAAT AGGGGTGACCC GTCGTGGTG

4601 ACGAACCCCC CGTTCAGGCC GACCGCTGCG CCTTATCCGG TAACTATCGT CTGAGTCCA ACCCGGTAAAG ACACGACTTA TCGCCACTGG CAGCAGCCAC  
TGCTTGGGG GCAAGTGGG CTGGCACCGC GGAATAGGCC ATTGATAGCA TCCGCCACCA TCCAGCAAGC GAGGTTCGACCC GTCGTGGTG

4701 TGGTAACAGG ATTAGCAGAG CGAGGTATGT AGGGGGTGT ACAGAGTTCT TGAAGTGGT GCCTAACTAC GGCTACACTA GAGGGACAGT ATTGTTGATC  
ACCATTTGTC TATCTGTC GCTCCATACA TCCGCCACCA TGTCTCAAGA ACTTCACCA CGGATTGAT CGCATGTGAT CTCCTGTCA TAAACATAG

4801 TGGGCTCTGC TGAAGGCCAGT TACCTTCGGA AAAAGAGTGT GTAGCTCTTG ATCCGGCAA CAAACACCG CTGGTAGGG TGGTTTTT GTTTCGAAGC  
ACGGAGACG ACTTCGGTCA ATGGAAGCCT TTTCAGGCTT CATCGAGAAC TAGGCCGTTT GTTGGTGGC GACCATCGCC ACCAAAAAA CAAACGTTG

4901 AGGAGATTAC GCGCAGAAA AAAGGATCTC AAGAAGATCC TTTGATCTT TCTACGGGGT CTGACGCTCA GTGGAACGAA AACTCACGT AAGGGATT  
TCGTCTAATG CGGGTCTTT TTTCCCTAGAG TTCTCTAGG AACTAGAAA AGATGCCCA GACTGCGAGT CACCTGTCTT TGAGTGCMA TTCCCTAAA

5001 GGTCAATGAGA TTATCAAAA GGATCTCAC CTAGATCCTT TAAATTTAA AATGAGTTT TAAATCAATC TAAAGTATAT ATGAGTAAC TTGGTCTGAC  
CCAGTACTCTT AATAGTTTT CCTAGAAGTG GATCTAGAA ATTAAATT TTACTTCAA ATTAGTTAG ATTCAATA TACTCATTTG AACCAAGACTG

5101 AGTTTACCAAT CCTTTAATCAG TGAGGGCACCT ATCTCAGGA TCTGTCTTATT TCGTTCATCC ATAGTTGCC GACTCCCCGT CGTGTAGATA ACTAGATA  
 TCAATGGTTA CGAATTAGTC ACTCCGTGG AGACAGATAA ACCAAGTAGG TATCAACGG CTTGAGGGCA GCACATCTAT TGATGCTAT  
  
 5201 GGGAGGGCTT ACCATCTGGC CCCAGTGGC CAAATGATACC GCGAGACCCA CGCTCACCGG CTCCAGATT ATCAGCAATA AACCAGCCAG CGGGAAAGGGC  
 CCCCTCCGAA TGGTAGACCG GGGTCAACG CTTACTATGG CGCTCTGGGT GCGAGTGGCC GAGGTCTAAA TAGTCGTTAT TTGGTCGGTC GGCCTTCCCG  
  
 5301 CGAGGGCAGA AGTGGTCCCTG CAACTTTATC CGCCTCCATC CAGTCTTATT ATTGTTGCCG GGAAGCTAGA GTAGTGTATT CGCCAGTTAA TAGTTGCGC  
 GCTCGGTCT TACCAAGGAC GTTGAATAG GCGGAGCTAG GTCAGATAAT TACAACGGC CCTTCGATCT CATTCAAA GGGTCAATT ATCAAACGCG  
  
 5401 AACGTTGTTG CCATTCGTC AGGGATCCTG GTGTACGGT CGTCGTCTGG TATGGCTTCA TTCAAGCTCCG GTTCCAAACG ATCAAGCGA GTTACATGAT  
 TTGCAACG GGTAAACGAG TCCGTAGGCAC CACAGTGGCA GCAGCAAAC ATACCGAAAGT AAGTCGAGGC CAAGGGTTCG TAGTTCCGCT CAATGCTACTA  
  
 5501 CCCCCATGTT GTGCAAAAAA GCGGTTAGCT CCTTCGGTCC TCCGATCGTT GTCAAGAAGTA AGTTGGCCGC AGTGTATCA CTCAAGGTTA TGGCAGGACT  
 GGGGTACAA CACGTTTTT CGCCAAATCGA GGAAGCCAGG AGGCTAGCAA CAGGTTCAAT TCACAAATAGT GAGTACCAAT ACCGTCGTGA  
  
 5601 GCATAAFTCT CTACTGTCA TGCCATCCGT AAGATGCTT TCTGTGACTG GTGAGTACTC ACCAAGTCA TTCTGAGAAT AGTGTATGGC GCGACCGAGT  
 CGTATTAAAGA GAATGACAGT ACGGTAGGCA TTCTACGAAA AGACACTGAC CACTCATGAG TTGGTTCACT AAGACTCTTA TCACATAACGC CGCTGGCTCA  
  
 5701 TGCTCTGGC CGGGTCAAC ACCGGATAAT ACCGGCCAC ATAGGAAAC TTAAAAGTG CTCAATCATTG GAAAAGTTC TTICGGGGCA AAACCTCAA  
 ACAGGAACGG GCGCAGTTG TGCCCTATTAGG TATGTCCTG AAATTTCACT GAGTACTAAC CTTTGCAAG AAGCCCCGCTT TTGAGACTT  
  
 5801 GGATCTTACCGC GGTGTGAGA TCCAGTTCGA TGTAAACCCAC TCGTGCACCC AACTGATCTT CAGCATCTT TACTTTCACTT AGCGTTCTG GGTGAGCAA  
 CCTAGAATGG CGACAACACTCT AGGTCAAGCT ACATGGGTG AGCACGTGGG TTGACTAGAA GTCTGAGAAA ATGAAAGTGG TCGCAAAGAC CCACTCGTT  
  
 5901 AACAGGAAGG CAAAATGCCG CAAAAAAGGG AATAAGGGG ACACGGAAAT GTGAAATACT CATACTCTC CTTTTCAAT ATTATTGAAG CATTATCAG  
 TTGTCCTTCCG TTTCACGGC TTATTCGGC TTGACTATGAA CAACTATGAA GTATGAGAAG GAAAGTGA TATAACTTC GTAAATAGTC  
  
 6001 GGTTATGTC TCATGAGCGG ATACATATT GAATGTTATT AGAAAATAA ACATAATAGGG GTTCGGGCCA CATTTCGGCA AAAAGTGCCA CCTGAGCTCT  
 CCAAATACAG AGTACTCGCC TATGTTAAA CTTACATAAA TCTTTCACGGT CAAGGGCGT GTAAAGGGC TTTCACGGT GGACTGCGAGA

101 AAGAAACCAT TATTATCATG ACATTAACCT ATAAAATAG GCGTATCAGG AGGCCCTTC GTCTTCATAA CAGGTAGACC TTTCGTAGAG ATGTACAGTG  
TTCTTGGTA ATATAGTAG TGTAATTGGA TATTTTATC CGCATAGTGC TCCGAAAG CAGAAGTTAT GTCCATCTGG AAAGCATCTC TACATGTCAC

201 AAATCCCGA AATTATACAC ATGACTGAGA GAAGGGAGCT CGTCATTCCC TGCGGGTTA CGTCACCTA CATCACTGTT ACTTTAAAAA AGTTTCCACT  
TTTAGGGCT TAAATATGTG TACTGACTTC CTTCCCTCGA GCAGTAAGGG AGCCCAAT GCAGTGGATT GTAGTGACAA TCAAAGGTGA

301 TGACACTTG ATCCCTGATG GAAAACGGCAT AATCTGGAC AGTAGAAAAGG GCTTCATCAT ATCAAATGCA ACGTACAAAG AAATAGGGCT TCTGACCTGT  
ACTGTGAAAC TAGGGACTAC CTTTGGCTA TTAGACCTG TCATCTTCCC CGAAGTAGTA TAGTTACGT TGCAATGTTTC TTATCCGA AGACTGGACA

401 GAAGGAAACAG TCAAATGGCA TTGTATAG ACAAACTATC TCAACACATCG ACAAAACAT ACAATACAGG TAGACCTTC GTAGAGATGT ACACTGAAAT  
CTTCGGTGTG AGTAACTCCGT AAACATATTC TGTTGTATAG AGTGTGTAGC TGTTGGTTA TGTTATGTTC ATCTGAAAG CATCTCTACA TGTCACTTA

501 CCCCCAAATT ATACACATGA CTGAAGGAG GGAGCTCGTC ATTCCCTGCC GGGTTACGTC ACCTAACATC ACTGTIACTT TAAAGGTT TCCACTTGAC  
GGGGCTTAA TATGTTGACT GACTTCCTTC CCTCGAGGAGC TAAAGGACGG CCCAATGCCAG TGGAATGCG AGGTGAACT

601 ACTTTGATCC CTGATGGAA ACCGATATTC TGGGACAGTA GAAAGGGCTT CATCATATCA ATGCAACGT ACAAAAGAAT AGGGCTCTG ACCTGTGAAG  
TGAAACTAGG GACTACCTT TGCGTATAG ACCCGTCACT CTTTCCCGAA GTAGTATAGT TAAAGGTTAG TGCAATGAA ATTTCCTCAA AGGTGAACTTC

701 CAAACAGTCAA TGGGATTG TATAAGACAA ACTATCTCAC ACATCGACAA ACCAACACAA TCTTACAGGT TGTTATGTT AGATGTCCAT TGTTCTTAA  
GTGTCAGTT ACCCGTAAAC ATATTCTGT TGATAGAGTG TGTTAGCTGT TGTTATGTT AGATGTCCAT TGTTCTTAA TGCAACTTC

801 CGGAAATTAT ACACATGACT GAAGGAAGGG AGCTCGTCAT TCCCTGCCG GTTACGTCAC CTAACATCAC TGTTACTTAA AAAAGTTTC CACTTGACAC  
GGCTTTAATA TGTCAGTCA CTTCCCTCCC TCGAGGAGTA AGGGACGGCC CAATGAGTG GATTGAGTG ACAATGAAAT TTTCCTCAAAG GTGAACACTG

901 TTGATCCCT GATGAAAC GCATAATCTG GGACAGTGAAGGGCTTCAC TCAATACAA TGAAACGTAC AAAGAAATAG GGCTTCTGAC CTGTGAAGCA  
AAACTAGGGAA CTACCTTTCG CGTATTAGAC CCTGTCACTT TCCCGAAGT AGTATAGTT ACGTGCTTAC CGGAAAGACTG GACACTTCGT

101 ACAGTCATG GGCATTTGTA TAAGACAAAC TATCTCACAC ATGCACAAAC CAATACAATC  
TGTCACTTAC CGTAAACAT ATTCTGTTG ATAGAGTGTG TAGCTGTTTG GTTATGTTAG

1 GAATTCAACT TCTCCATACT TTGGATAAGG AATAACAGAC ATGAAATACT TCATTCGTA GTTGTATTTCGTTA AGCTTGGCC AAAAGAGA AGAGTCGAAT  
CTTAAGTTGA AGAGGTATGA AACCTATTCC TTATATGCTG TACTTTAG AGTAACGACT CAACAATAAA TTGGAACGGG TTTTTCTCT TCTCAGCTTA

101 GAACTGTGT CGCAGGTAGA AGCTTGGAG ATTATCGCA CTGCAATTGCT TCCCAATTG GCGAAATG ACCAACAGGG GTTGATTGAT CAGGTAGGG  
CTTGACACAC GCGTCACATCT TCGAACCTC TAATAGCAGT GACGTATGA AGCGTTATAC CGCGTTTAC TGCTTGTGC CAACTAACTA GTCCATCTCC

201 GGGGCTGTGA CGAGGTAAGS CCCGATGCCA GCAATTCTGA CGACGATACG GAGCTGTGC GCGATTACGT AAAGAAGTAA TTGAAGCATC CTGCTGAGA  
CCCGGACAT GCTCCATTTC GGGCAGGT CGTAAGGACT GCTGCTATGC CTOGACGACG CGCTAATGCA TTCTCAAT AACCTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTCAACA GCTGTCAAA AGTTGTCAAGG GCCGAGACTT ATAGTCGCTT TGTTTATTTCGTTT TTGTAACTA GTACCGCAAGT  
TTTCAATTAA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGGCTGTGAA TATCAGCGAA ACAAAATAA AAAATTACAT AACATTTGAT CATGGTCTTA

401 TCACGTAAAA AGGGTATGTA GAGGTGAGG TGATTTATG AAAAGATA TCGATTTCGTT TCTTCGATCT ATGTCGTTT TTTCCTATGTC TACAAATGCC  
AGTGCATTTC TCCCATACT CTCCAACTCC ACTAAATAAC TTTCCTTAT AGCTAAAGA AGAACGTAGA TACAAAGCAA AAAGATAACG ATGTTACGG  
1

M K K N I A F L I A S M F V F S I A T N A  
^ start of stII sequence

501 TATGGATCCG ATATCCAGAT GACCCAGTCC CCGAGCTCCC TGTCCGCCCTC TGTTGGCGAT AGGGTCACCA TCACCTGCCG TGCCAGTCAG GATGTTCCA  
ATACGGTAGGC TATAGGTCTA CTGGTCTA CTGGTCTAGT GTCTTGGTC CTTTCGAGG ACAGGGGG ACCTGGTCTGGT AGTGGACGGC ACGGTCAGTC CTACACAGGT  
22 Y A S D I Q M T Q S P S L S A S V G D R V T I T C R A S Q D V S T  
^ light chain start

601 CTGGCTGTAGC CTGGTATCAA CAGAAACCAAG GAAAGCTCC GAAGCTTCTG ATTACTCGG CATCCTTCCT CTACTCTGG GAATTCAGCAAT CTTCTCTGG  
GACGACATCG GACCATAGT GTCTTGGTC CTTTCGAGG CTTATGAGCC GATGAGACCT CAGGGAAAGAG CGAAGAGACC  
56 A V A W Y Q K P G K A P K L I Y S A S F L Y S G V P S R F S G  
^ CDR-L1

701 TAGGGTTCC GGACGGATT TCACTCTGAC CATCAGGAGT CTGCAGCCGG AAGACCTCGC AACTTATTAC TGTAGCAAT CTTATACTAC TCCTCCACCG  
ATGCCAAAGG CCCTGCCTAA AGTGAGACTG GTAGTCGTCA GACGTGGCC TTCTGAAGCG TTGAATATG ACAGTCGTTA GAATATGATG AGGAGGGTGC  
89 S G S G T D F T L T I S S L Q P E D F A T Y Y C Q Q S Y T T P P T  
^ CDR-L2

**FIG. 26A**

1 TTCGGACAGG GTACCAAGGT GGAGATCAA CGAACTGTGG CTGGACCATC TGTCCTCATC TTCCGCCAT CTGATGAGCA GTTGAATCT GGAACGTGCT  
2 AAGCCCTGTC CAGGGTCCA CCTCTAGTT GCTTCAGACC GACGTGGTAG ACAGAACTAG MGGGGGGTA GACTACTGT CAACTTTAGA CCTTGACGGA  
2 F G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S

1 CTGTTGTGTG CCTGGAAAT AACTCTATC CCAGAGGGC CAAAGTACAG TGGAAAGGTGG ATAAGCCCT CCAATCGGGT AACTCCAGG AGAGTGTGAC  
2 GACAACACAC GGACGACTTA TGAAAGATAG GGTCTCTCG GTTCATGTC ACCTTCACC TATTCGGGA GGTTAGCCCA TTGAGGGTCC TCTCACAGTG  
6 V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T

1 AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC ACCCTGACGC TGAGCAAAGC AGACTACAG AAAACACAAAG TCTACGCCCTG CGAAGTCACC  
2 TCTCGTCTG TGTTCTGT CGAGTCGTG CGTGGATGTC GGAGTCGTG TGGAAGCTGCG ACTCGTTCG TCTGATGCTC TTGTGTGTT AGATGGGAC GCTTCAGTGG  
9 E Q D S R D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T

1 CATCAGGGCC TGAGGCTGCC CGTCACAAAG AGCTTCACAA GGGGAGACTG TGGGAGACTG TCCGGTATGG CTCGATCCCAA CCGTTCCGG CCGTAAGGCC  
2 GTAGTCCGGG ACTCGAGGG GCAGTGTTC TCGAAGCTGT CCCCTCTCAC ACCACGGTGG AGGCCATACC GACTAGGGCTT GGCAAAGGGCG CCATTCCGG  
2 H Q G L S S P V T K S F N R G E C G A S S G M A D P N R F R G K D I  
^end of light chain, start of gd tag

25/75

1 TGGCATAACT CGAGGGCTGAT CCTCTACGCC GGACGATCG TGGCCCTAGT ACGCAAGTTC ACGTAAAAAG GTAACTAGA GTTGAAGGTG ATTATATGAA  
2 ACCGTATTGA GCTCCGACTA GGAGATGCCG CCTGCGTAGC ACCGGGATCA TGGTTCAAG TGCATTTTTC CCATTGATCT CCAACTCCAC TAAATACCT  
6 A O  
3 M K  
^start of stII

1 AAAGAATATC GCATTCTTC TTGCACTATGTTT GTTATTGCTA CAAACGGTA CGCTGAGGT CAGCTGGTGG AGTCCTGGGG TGGCTGCTGG  
2 TTCTTATAG CGTAAGAAG AACGTAGATA CAAGCAAAA AGATAACGAT GTTGTGCGAT GCGACTCCAA GTGACCCACC TCAGACGCC ACCGGACCA  
1 K N I A F L I A S M F V F S I A T N A Y A E V Q L V E S G G G L V  
^start of heavy chain

1 CAGCCAGGG GCTCACTCCG TTGCTCTGT GCAGCTCTGT GCTCAACAT AAAAGACACC TATATACACT GGGTGGTCA GGGCCGGGT AGGGCCTG  
2 GTCGGTCCC CGAGTGGGC AAACAGGACA CGTCGAAGAC CGAGTGTGA ATATATGTGG ATATATGTGA CCCACGCACT CGGGGGCCA TTCCCGGAC  
3 Q P G G S I R L S C A A S G F N I K D T Y I H W V R Q A P G K G L E  
^CDR-H1

FIG. 26B

1501 AATGGGTTGC AGGAGTTTAT CCTACCAATG GTTACTAG ATATGCCGAT AGCGTCAAGG GCCGTTCAC TATAAGCGCA GACACATCA AAAACACAGC  
 TTACCCAACG TTCCCTAAATA GGATGGTTAC CAATATGATC TATAAGGCTA TCGCAGTTC CGGCAAGTGT ATATCGCGT CTGTGTAGGT TTGTGTGCG  
 47 W V A R I Y P T N G Y T R Y A D S V K G R F T I S A D T S K N T A  
 ^CDR-H2

1601 CTACCTACAA ATGAAACAGCT TAAGAGCTGA GGACACTGCC GTCTATTATT GTAGCCGCTG GGGAGGGAC GGCTCTATG CTATGGACTA CTGGGGTCAA  
 GATGGATGTT TACTTGTGAA ATTCTCGACT CCTGTGACGG CAGATAATAA CATCGGAC CCCTCCCTG CCGAAGATAC GATACTGTAT GACCCAGTT  
 80 Y L Q M N S L R A E D T A V Y Y C S S R W G G D G F Y A M D Y W G Q  
 ^CDR-H3

1701 GGAACACTAG TOACCGCTTC CTCGGCTCC ACCAAGGGCC CATCGGTCTT CCCCTCTGGCA CCCTCCTCCA AGAGCACCTC TGGGGGACA GCGGCCCTGG  
 CCTTGTGATC AGGGGAGG GAGGGCAGAG GTAGCCAGAA GGGGACCGT GGGAGGGGT TCTCGTGGAG ACCCCCGTGT CGCCGGGACC  
 113 G T L V T V S S T K G P S V F P L A P S K S T S G G T A A L G

1801 GCTGCCCTGGT CAAGGACTAC TTCCCCAAC CGGTGACGGT GTCGTGGAAC TCAAGGGCCC TGACCCAGGG CGTGCACACC TTCCCGGTG TCCTACAGTC  
 CGACGGACCA GTTCCGTATG AAGGGGCTTG GCACTGCCA CAGCACCTG AGTCCGGGG ACTGGTCCGC GCACGTGTGG AAGGGGCCAC AGGATGTGAG  
 147 C L V K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S

26/75

1901 CTCAGGACTC TACTCCTCA GCAGCGTGGT GACCGTGGCC TCCAGCAGCT TGCAACGTGA ATCACAGCC CAGCAACACC  
 GAGTCCGTGAG ATGGGGAGT CGTCGACCCA CTGGCACGGG AGGTGTCGA ACCCGTGGGT CTGGATGTAG ACGTGCACT TAGTGTGG GTCGTGTGG  
 180 S G L Y S L S S V V T V P S S S L G T Q T Y I C N V N H K P S N T

2001 AAGGTGACA AGAAAGTGA GCCCAAATCT TGTGACAAA CTCACGGCG CATGAAACAG CTAGAGGACA AGGTGAAAGA GCTACTCTCC AAGAACTACC  
 TTCCAGCTGT TCTTTCAACT CGGGTTAGA ACAGTGTGTT GAGTGGGGC GTACTTGTGTC GATCTCTGT TCCAGCTCTC GATGAGAGG TTCTTGATGG  
 213 K V D K K V E P K S C D K T H G R M K Q L E D K V E E L L S K N Y H

^end of heavy chain, start of leucine zipper

2101 ACCTAGAGAA TGAAGTGGCA AGACTCAAAA AACTTGTGG GGAGCGGCA AAGCTTAGTG GCGGTGGCTC TGGTCCGGT GATTGTGATT ATGAAAGAT  
 TGGATCTCTT ACTTCACCGT TCTGAGTTT TTGAAACAGCC CCTCGGCCCT TTGGAATCAC CGCCACCGAG ACCAAGGCCA CTAAGCTAA TACTTTCTAA  
 247 L E N E V A R L K K L V G E R G K L S G G S G S G D F D Y E K M  
 end of leucine zipper, start of gene III coat protein (267-end)

FIG. 26C

2201 GGC<sub>3</sub>AAACGCT ATAAGGGGG CTATGACCGA AAATGCCGAT GAAACGCCG TACAGTCTGA CGCTAAAGGC AAACTTGATT CTGTCGCTAC TGATTAACGGT  
CCGTTGCGA TTATTCCCCC GATACTGGCT TTTACGGCTA CTTTGGCTT GATGCAAGCT GCGATTTCG TTTGAACAA GACAGGGATG ACTATGCCA  
280 A N A N K G A M T E N A D E N A L Q S D A K G K L D S V A T D Y G

2301 GCTGGCTATCG ATGGTTTCAT TGGTGCAGTT TCCGGCCTTG CTAATGGTAA TGTTGCTACT GGTGATTTCG CTGGCTCTAA TTCCCAATG GCTAAAGTCG  
CGACCGATAGC TACCAAGTA ACCACTGCAA AGGGCGAAC GATTACCAATT ACCACGATGA CCACTAAAC GACCGAGATT AGGGGTTAC CGAGTCAGC  
313 A I D G F I G D V S G L A N G N G A T G D F A G S N S Q M A Q V G

2401 GTGACGGTGA TAATTCACTT TTAATGAAATA ATTTCACCT TCCCTCCCTC AATCGGTGA ATGTCGCCCT TTTGTCTTA GCGCTGGTAA  
CACTGCCACT ATTAAGTGA AATTACCTT TAAAGGCAGT TATAATGGA AGGGGGAG TTAGCCAAT TACAGGGGA AACAGAAAT CGCGACCAT  
347 D G D N S P L M N N F R Q Y L P S L P Q S V E C R P F V F S A G K

2501 ACCATATGAA TTTCTATG ATTGTACAA AATAAACTTA TICCGTGGT TCTTGTATAT GTGCCACCT TTATGTATGT ATTTCCTACG  
TGTGTATCTT AAAAGATAAC TAACACTGT TTATTTGAAT AAGGCCAAC AGAAACGAA AGAAATATA CAACGGTGA AATACATACA TAAAGATGC  
380 P Y E F S I D C D K I N L F R G V F A F L L Y V A T F M Y V F S T

2601 TTGCTAAACA TACTGGCTAA TAAGGAGCT TAATCATGTC AGTTCTTTTG GCTAGGCCG CCCTTATACCT TGTCTGCCTC CCCGGCTGCG  
AAACGATTGT ATGACGCCATT ATTCCCTAGA ATTGTACGG TCAAGAAAAC CGATGCCGG GGGATATGGA ACAGACGGG GGGGCCAACG CAGGCCACG  
413 F A N I L R N K E S O

2701 ATGGAGCCG GCCACCTCGA CCTGATGGA AGCCGGCGGC ACCTCGCTAA CGGATTCAAC ACTCCIAAGAA TTGGAGCCAA TCAATTCTTG CGGAGAACTG  
TACCTCGGCC CGTGGAGCT GGACTTACCT TCGGGCGCCG TGGAGCGATT GCTAAGTGG TGAGGTCTT AACCTCGTT AGTAAGAAC GCCTCTGAC

2801 TGAATGGCA ACCAACCTT TGGCAACA TATCCATCGC GTCCGCCATC TCCAGCAGCC GCACGCCGG CATCTCGGG ACGGTTGGGT CCTGCCACG  
ACTTACCGCT TTGCTGGGA ACCGTCCTGT ATTAGTAGCG CAGGGTAG AGTCGTCGG CGTGGCCCG GTAGAGCCCG TCGAAACCCA GGACGGTGC  
4775

2901 GGTGGCATG ATCGTGCCTC TGTGTTGAG GACCCGGCTA GGCTGGGG GTGCTGCTTAC TGGTTAGCAG AATGAATCAC CGATAACGGGA GCGAACGTGA  
CCACGGGTAC TAGCACGAGG ACAGCAACTC CTGGGGCGAT CGAACGGCCC CAACGGAATG ACCAATCGTC TTACTTAGTG GCTATGGCT CGCTTGACT

3001 AGCGACTGGCT GCTGCCAAC ACCTGGGACC TGGCAACAA CATGAATGGT CTTCGGTTTC CGTGGTCTGT AAAGTCTGGA AACGGGGAG TCAGGGCCT  
TCGCTGACGA CGACGTTTGT CAGACGCTGG ACTCGTGTGT GTACTTACCA GAAGCCAAG GCACAAAGCA TTTCAGACCT TTGGCCCTTC AGTCGCCAGA

FIG. - 16 D

3101 GCACCAATTAT GTTCCGGATC TGCATCGCAG GATGCTGCTG GCTACCCTGT GGAAACACCTA CATCTGTATT AACGAAGGCC TGGCATTTGAC CCTGGACTGAT  
CGTGGTAATA CAAGGCTTAG ACGTAGCGTC CTACGACGAC CGATGGGACA CCTTGGGAT GTAGACATA TTGCTTCGGG ACCGTAACTG GGACTCACTA

3201 TTTTCTCTGG TCCATACCGC CAGTGTATT CCCTCACAAAC GTTCCAGTAA CGGGCATGT TCATCATCAG TAACCCGTAT CGTGGACATC  
AAAAGAGACC AGGGGGCGT AGGTATGGG GTCAACAAAT GGGAGTGTG CAAGGTCTATT GCCCCTGACA AGTGTAGTC ATTGGGATA GCACTCGTAG

3301 CTCTCTCGTT TCATCGGTAT CATTACCCC ATGAAACAGAA ATTCCCGCTT ACACGGAGGC ATCAAGTGCAC CAAACAGGA AAAACCGCCC TTAAACATGGC  
GGCGAAATAG TCTTCGGTCT GTAAATGGGG TACTTGTCTT TAAGGGGAA TGTGCCCTCG TACTTCAGT GTTGTCCCTT TTITGGGGG ATTGTACCG

3401 CCGCTTTATC AGAAGCCAGA CATTAAACGCT TCTGGAGAA CTCAACGAGC TGGACGGGA TGAACAGGCA GACATCTGTG AATCGCTICA CGACACAGCT  
CTACTCGAAA TGGCGTCCATA GGCCCTTAAC ATTGGCAATT ATAAACAT TTAAAGGCCA ATTAAAAC ATTGTAGTC TTAGCGAAGT GCTGGTGGGA

3501 GATGAGCTT ACCGGAGGAT CCGGAAATTG TAAACGTATA TATTGTGTA AAATTGGGT TAAATTTG TTAAATCAGC TCATTTTTA ACCAATAGGC  
GCTTTAGCCG TTGTAGGAA TATTAGTGT TCTTATCTGG CTCTATCCC ACTCACAAAC AGGTCAAAACC TTGTCTTCAG GTGATAATT AGTAAAAAT TGGTTATCCG

3601 CGAAATCGGC AAATCCCTT ATAATCAA AGAATAGACCC GAGATAGGGT TGAGTGTGT TCCAGTTGG AACAGAGTC CACTATAAA GAACGTGGAC  
GCTTTAGCCG TTGTAGGAA TATTAGTGT TCTTATCTGG CTCTATCCC ACTCACAAAC AGGTCAAAACC TTGTCTTCAG GTGATAATT CTTGCACTCG

3701 TCCAACGTCA AAGGGGAAAA AACCGTCTAT CAGGGCTATG GCCCACTACG TGAACCATICA CCCTAATCAA GTTTTTGG GTCGAGGTGC CGTAAGGCAC  
AGGTGGAGT TTCCCGCTTT TTGGCAGATA GTCCGATAC CGGGGTATGC ACTTGGTAGT GGGATTAGTT CAAAAACCC CAGCTCCACG GCATTTCGTG

3801 TAAATGGAA CCTAAAGGG AGCCCCCGAT TTAGAGCTT CAGGGAAAG CGGGGAACG TGGCGAGAA GAAGGGAAAG AAAGGAAAG GAGGGGGCG  
ATTTTAGCCTT GGATTTTCCC TCGGGGCTTA AATCTCGAAC TGGCGCTTT GGCCTGCTTC ACCGCTCTTC CCTTCCCTTC TTTCGCTTTC CTCGCCCGCG

3901 TAGGGGCTG GCAAGTGTAG CGGTCAAGC ACCACACCCG CCGCGCTTA TGGCGCCGTA CAGGGCGGT CCTGGATCTG CCTGGCGGT  
ATCCCCGAC CGTCACATC GCCAGTGCAGA CGGGCATTTG TACGTGAGG GGGCGGAATT ACGGGGCAT GTCCCGCGCA GGCCTAGGAC GGAGGGCGCA

4001 TTGGGTGATG AGGTGAAA CCTCTGACAC ATGGAGCTCC CGGAGACGGT CACAGCTGT CTGTAAGGG ATGCGGGAG CAGACAAGCC CGTCAGGGCG  
AAGCCACATC TGCCACTTT GGAGACTGT TACGTGAGG GCCTCTGCCA GTGTGAAACA GACATTGCC TACGGCCCTC GTCTGTTCGG GCAGTCCCG

4101 CGTCAGGGGG TTGTTGGGGG TGTGGGGCG CAGCCATGAC CCAGTCACGT AGCGATAGGG GAGTGTATAC TGGCTTAAC ATGGCCATC AGAGGAGATT  
GCAGTGGCCC ACAACCGCCC ACAGCCCGCG GTCGGTACTG GGTCACTGC CTCACATATG ACCGAAATTGA TACGCCGTAG TCTCGTCTAA

4201 GTACTGAGAG TGCACCATAT GCGGTGTGAA ATACCGCACA GATGCCATAAG GAGAAATAAC CGCATCAGGC GCTCTCCGC TTCCTCGCTC ACTGACTCGC  
CATGACTCTC ACGTGCTATA CGCCACACTT TATGGCGTGT CTACGGATT CTCTTATG GCCTAGTCGG CGAGGAAGGC AGAGGGAG AGAACATGTG

4301 TGGCGCTCGGT CGTTCGGCTG CGGCAGCCGG TATCAGCTCA CTCAAAGGGG GTATAACGGT TATCCACAGA ATCAGGGAT AACGAGGAA AGAACATGTG  
ACGGGAGCCA GCAAGCCGAC GCGGCTGCC ATAGTCGAGT GAGTTTCCGC CATATGCCA ATAGTCGAGT TATGCTCTCTA TGTCTGACAC

4401 AGCAAAAGGC CAGCAAAGG CCAGGAACCG TAAAAAGGCC GCGTTGCTGG CGTTTTCCA TAGGCCCTGAG CCCCTGAGC AGCATCACAA AAATCAGGC  
TCGTTTTCGG GTCTGTTTCCG GTCAGGCTTCCG ATTTTTCGG CGCAACACC GCAAAAGGT ATCCGAGGGG GGGGACTGTC TGTAGTCGTT TTAGCTGGC

4501 TCAAGTCAA GGTGGCGAAA CCCGACAGGA CTATAAAGAT ACCAGGGTT TCCCTGGAA AGCTCCCTCG TGGCTCTCC TGTCCGACC CTGCGCTTA  
AGTTCTAGTCT CCACCGCTTT GGGCTGTCTT GATAATTCTA TGGTCCGAA AGGGGACCT TGAGGGAGGC ACGGAGAGG ACAAGGCTGG GACGGGAAT

4601 CCGGATACCT GTCCGCCTT CTCCCTCTCGG GAAGCGTGGC GTTCTCTCAT AGCTCACGGT GTAGGTATCT CAGTCGGT TAGGTCTGTC GCTCCAGCT  
GGCCTATGGAA CAGGGAGCC CTTCGGACCG CGAAAGAGTA TCGAGTGGCA CATCCATAGA GTCAAGCCAC ATCCAGCAAG CGAGGTTGCA

4701 GGGCTGTGTG CACGAACCCC CCGTTCAAGCC CGACCGCTGC GCCTTATCCG GTAACTATCG TCTTGAGTCC AACCCGGTAA GACAGCACT ATGGCACTG  
CCCGACACAC GTGCTTGGGG GCGAAGTCGG GCTGGCGACG CGGAATAGGC CATTGATAGC AGAACTCAGG TTGCGCCATT CTGTGCTGAA TAGGGTGCAC

4801 GCAGCAGCCA CTGGCTAACAG GATTAGCAGA GCGAGGTATG TAGGGGGTC TACAGAGTTC TGAAGTGGT GGCCTAACTA CGGCTACACT AGAAGGACAG  
CGTCGTCGGT GACCATTTGTC CTAATCGTCT CGCTCCATAC ATCCGCCACG ATGTCCTAACG AACTTCACCA CGGGATTGAT GCGCATGTA TCTTCCTGTC

4901 TATTGGTAT CTGGCTCTG CTGAAGCCAG TTACCTTCGG AAAAGAGTT GTAGCTCTT GATCCGGCAA ACAMACCACC GCTGGTAGCG GTGGTTTTT  
ATAAACATA GACGGAGAC GACCTGGTC AATGGAAGCC TTTCTCAA CCATCGAGA CTAGGGCTT TGTTGGTGG CGACCATCGC CACCAAAA

5001 TGTGGTGCAG CAGCAGATA CGCGAGAAA AAAAGGATCT CAAGAAGATC CTTGATCTT TTACGGGG TCTGAGGCTC AGTGAACGA AACTCACGT  
ACAAACCTTC GTCTGCTAAT GCGGCTCTT TTTCCTAGA GTTCTCTAG GAAACTAGAA AAGATGCCAG TCAACCTGGT TTGGAGTGC

5101 TAAGGGATT TGGTCATGAG ATTATCAAA AGGATCTCA CCTAGATCTT TTAAATAAA AATGAGTT TAAACTAACTA TATGAGTAA  
ATTCCTAAA ACCAGTACTC TAATGTTT TCCTAGAAGT GGATCTAGGA AAATTAAATT TTACTTCAA AATTAGTTA GATTTCATAT ATACTCTT

5201 CTTGGTCTGA CAGTACCAA TGCTTAATCA GTGAGGCACC TATCTCAGGG ATCTGCTAT TCGCTCCGC TGAAGTCCCG TCGTGTAGAT  
GAACCAAGACT GTCAATGGTT AGCAATTAGT CACTCCGTGG ATAGAGTCGG TAGACAGATA AGCAAGTAGT GTATCAACGG ACTGAGGGGC AGCACATCTA

5301 AACTACGATA CGGGGGGCT TACCATCTGG CCCCACTGGT GCAATGATAAC CGCGAGACCC ACGCTCACCG GCTCCAGATT TATCAGCAAT AACCCAGCCA  
TTGATGCTAT GCCCTCCGA ATGGTAGACC GGGGTACCGA CGTTACTATG CGCCTCTGGG TGCAGTGGC CGAGGTCTAA ATAGTCGTTA TTTGGTCGGT

5401 GCCGGAAAGG CCGAGCCAG AAGTGTCTCTT GCAACTTAT CGGCCTCCAT CCACTCTATT AATTGTTGCC GGGAAAGCTAG AGTAAGTGT TCGCAGTAA  
CGGCCCTCCC GGCTCGGTC TTCAACAGGA CGTTCAGATAA CGGTGAATAA CGGTGAAGGTA GGTCAAGATAA TTAAACACGG CCCTTCGATC TCATTCAICA AGGGTCAAT

5501 ATAGTTGCG CAACTGTTGT GCCATGCTG CAGGCCATCGT GGTGTACCG TCCTGCTGTTG GTATGGCTTC ATTCAAGCTCC GGTTCCCAAC GATCAAGGGC  
TATCAAACGC GTGCAACAA CGGTAAACGA CGTCCGTTAGCA CCACAGGAC AGCAGCAAAAC CATAACGGG TAAGTCGAGG CCAAGGGTGT CTAGTCGGC

5601 AGTTACATGA TCCCCATGT TGTGCAAAAA AGCGGTTAGC TCCTTGGTC CTCGGATCGT TGTCAAGT AAGTGGCCG CAGTGTATC ACTCATGGTT  
TCAATGTACT AGGGGGTACA ACACGGTTTT TCGCCAATCG AGGAAGCCAG GAGGTAGCA ACAGTCTCA TTCAACCGGC GTCAAAATAG TGAGTACAA

5701 ATGGCAGCAC TCCATAATTCTCTTACTGTC ATGCCATCG TAAGATGCTT TTCTGTGACT GGTGAGTACT CAACCAAGTC ATTCTGAGAA TAGTGTATGC  
TACCGTGTG AGCTTAAAG AGAATGACAG TACGGTAGGC ATTCTACGAA AAGACACTGA CCACTCATGA GTTGGTTAG TAAAGACTCTT ATCACATAAG

5801 GGCGACCGAG TTGCTCTTGC CGGGCGTCAA CACGGATAA TACCGGCCA CATAGCAGAA CTTTAAAGT GCTCATCATT GGAAACGTT CTTCGGGGCG  
CCGCTGGCTC AACGAGAACG GGCGCAAGT GTGCCCTATT ATGGCGGGT GTATCGCTT GAAATTCA CGAGTACTAA CCTTTTGCAA GAAGCCCGC

5901 AAAACTCTCA AGGATCTTAC CGCTGTGAG ATCCAGTTCG ATGTAACCCA CTCGTGCACC CAACTGATCT TCAGCATCTT TTACTTCAC CAGGTTCT  
TTTGAGAGT TCTTAAAGT GGCACAACTC TAGGTCAAGC TACATTGGGT GAGCACGTGG GTTGAATGAGA AGTGTAGAA ATGAAAGTG GTCGAAAGA

6001 GGGTGGCAA AAACAGGAAG GCAAAATGCC GCAAAAAAGG GAATAAGGG GACACGGAA TGTGAATAC TCATACTCTT CCTTTTTCAA TATTATTGAA  
CCCACTCGTT TTGTCCTTC CGTTTACGG CGTTTTTCC CGTTTTCGG CTGTGCCTTT ACAACTATG AGTATGAGAA GGGAAAAAGTT ATAATAACTT

6101 GCATTATCA GGTTTATTGT CTCATGGCG GATACATATT TGAATGATT TAGAAAATA AACAAATAGG GGTTCCGGC ACATTCCCC GAAAAGTGC  
CGTAAATAGT CCAATAACA GAGTACTCGC CTATGTATAA ACTACATAA ATCTTTTAT TGTGTATCC CCAAGGGCG TCTAAAGGG CTTTTACGG

6201 ACCTGACGTC TAAGAAACCA TTATTATCAT GACATAACC TATAAAATA GGCATATCAC GAGGCCCTT CGTCCTCAAT ACAGCTAGAC CTTTCGTTAGA  
TGGACTGCAG ATTCTTGGGT AATAATAGTA CTGTAATTGG ATATTTTAT CCGCATAGTG CTCCGGAAA GCAGAAGTT TGTCCATCTG GAAAGCATCT

6301 GATGACAGT GAAATCCCCG AAATTATACA CATGACTGAA GGAAAGGGC TCGTCATCC CTGGCGGGTT ACGTACCTA ACATCACTGT TACTTTAAA  
CTACATGTC CTTAGGGGC TTTAATATGT GTCAGTACTT CCTTCCTCG AGGAGTAAGG GACGGCCCA TGCAGTGGAT TGTACTGACA ATGAAATT

6401 AAGTTTCCAC TTGACACTT GATCCCTGAT GAAAACGCA TAATCTGGGA CAGTAGAAAG GGCTTCATCA TATCAAATGC AACGTACAAA GAAATAGGGC  
TTCAAAGGTG AACTGTGAAA CTAGGGACTA CCGTTTGCGT ATTAGACCCCT GTCACTTTC CGGAAGTAGT ATAGTTACG TTGATGTT CTTTATCCCG

6501 TTCTGACCTG TCAAAGCAACA GTCAATGGGC ATTGTGATAA GACAAACTAT CTACACATC GACAAACCA TACAATACAG GTAGACCTT CGTAGAGATG  
AAGACTGGAC ACTTCGTTGT CAGTAAACCG TAAACATATT CTGTTGATA GAGTGTAG CTGTTGGTT ATGTATGTC CATCTGGAAA GCATCTCTAC

6601 TACAGTGAAA TCCCAGAAAT TATACACATG ACTGAAGGAA GGGAGCTCGT CATTCCTGC CGGGTTACGT CACCTAACAT CACTGTTACT TTAAAAAAGT  
ATGTCACTTT AGGGGCTTTA ATATGTGTAC TGAACCTT CCCTCGAGCA GAAAGGGACG GCCCAGTCA GTGAGATGTA GTGACAATGA AATTTTTCA

6701 TTCCACCTGAA CACTTGTGATC CCTGTATGGAA AACGCATAAT CTGGGACAGT AGAAAGGGCT TCATCATATC AAATGCAACG TACAAAGAAA TAGGGCTCT  
AAGGTGAACCT GTGAAAACCTAG GGACTACCTT TTGGGTATTAA GACCCCTGTCA TCTTCCCGA AGTAGTATAG TTACGTGTC ATGTTTCTTT ATCCCGAAGA

6801 GACCTGTGAA GCAACAGTCA ATGGGCAATT GTATAAGACA AACTATTCAC CACATCGACA AACCAATACAA ATCTACAGGT AGACCTTTCG TAGAGATGTA  
CTGGACACTT CGTTGTCACTT TACCCGTTAA CATAATTCTGT TTGATAGAGT GTGATAGCTGT TTGGTTATGTT TAGATGTCCA TCTGGAAAGC ATCTCTACAT

6901 CACTGAAATC CCCGAATTAA TACACATGAC TGAAGGAAGG GAGCTCGTCA TTCCCTGCCG GTTACGTCA CCTAACATCA CTGTTACTT AAAAAGTT  
GTCACCTTGTGGCTTTAAT ATGTGTACTG ACTTCCTTCC CTCGAGCACTT AGGGGACGGC CCAATGCACTT GGATGTAGT GACAATGAAA TTTTTTCAAA

7001 CCACTTGACA CTTTGATCCC TGATGGAAA CGCAATAATCT GGGACAGTAG AAAGGGCTTC ATCATATCAA ATGCAACGTA CAAGAAATA GGGCTCTGA  
GGTGAACCTGT GAAACTAGGG ACTACCTTT GCGTATTAGA CCCTGTGTCATC TTTCGGAAAG TAGTATGTT TACGTGTCAT GTTCTTTAT CCCGAAGACT

7101 CCTGTGAAAGC AACAGTCAT GGGCATTTGT ATAAGACAAA CTATCTACA CATCGACAAA CCAATACAT C  
GGACACTTCG TTGTCAGTTA CCCGTAACAA TATTCGTTT GATAGAGTGT GTAGCTGTT GGTTATGTTA G

1 ATGAAAAAGA ATATCGCCATT TCTTCTTGCA TCTATGTTG 777777CTAT TGCTACAAAT GCCTATGCCAG ATATCCAGAT GACCCAGTCC CCGAGCTCCC  
 1 TACTTCTCTTCTATAGCGTAA AGAAGAACGT AGATACAAGC AAAAGATA ACAGATGTTA CGGATACGTC TATAGGTCTA CTGGGTCTAGG GGCTCGAGGG  
 1 M K N I A F L L A S M F V F S I A T N A Y A D I Q M T Q S P S S L  
 ^met  
 ^start of stII signal sequence

101 TGTCTGGCTC TGTGGGGAT AGGGTACCCA TCACCTGGCG TGCCAGTCAG GATGTTGTCGA CTGGTGTCCA CTGGTATCAA CAGAAACAG GAAAGCTCC  
 ACAGGGGAG ACACCCGCTA TCCCAGTGGT AGTGGACGGC ACGGTCTAGTC GACGACAGGT GACCATAGT GACGACATCG GACCATAGT GTCTTGGTC CTITTCGAGG  
 35 S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A P  
 ^CDR-L1

201 GAAGCTTCTG ATTACTCGG CATCCCTCTT CTACTCTGGA GTCCCTCTC GTCTCTCTGC TAGCGGGATT TCACTCTGAC CATAGGAGT  
 CTTCGAAGAC TAAATGAGCC GTAGGAAGGA GATGAGACTT CAGGGAAAGAG CGAAGAGACC ATCGCCAAAGG CCCTGCCAAAGG AGTGGAGCTG GTAGTCGTCA  
 68 K L I Y S A S F L Y S G V P S R F S G S G T D F T L T I S S  
 ^CDR-L2

301 CTGGAGCCGG AAGACTCTCGC AACTTATTAC TGTCTGCAAC ATTATACTAC TCCTCCACG TTGGACAGG GTACCAAGGT GGAGATCAAA CGAACTGTGG  
 GACGGTGGCC, TTCTGAGCG TTGAATAATG ACAGTCGTG TAATATGATG AGGAGGGTGC AAGCCTGTCC CATTGTTCCA CCTCTAGTT GCTTGACACC  
 101 L Q P E D F A T Y Y C Q Q H Y T T P P T F G Q G T K V E I K R T V A  
 ^CDR-L3

401 CTGGCACCAC TGTCTTCATC TTCCGCCAT CTGATGAGCA GTGAAATCT GAAACTGCCT CTGTTGGTG CCTGCTGAAT AACTTCATC CCAGAGGGC  
 GACGGTGGTAG ACAGAACTAG AAGGGGGCTA GACTACTGGT CAACTTAGA CCTTGACGGA GACAAACAC GGACGACTTA TTGAAGATAG GGTCTCTCCG  
 135 A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E A  
 ^CDR-L4

501 CAAAGTACAG TTGAAGGGG ATAACACAAAG TCTACGCCCT CCAATGGGT AACTCCAGG AGAGTGTACAG GCACCTACAG CCTCAGCAGC  
 GTTCTCATGTTC ACCTTCACCC TATTGGGGA GGTAGGCCA TTGAGGGTCC TCTCACAGTG TCTCGTCTGT CGTGGATGTC GGAGTCGTG  
 168 K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S S  
 ^CDR-L5

601 ACCCTGACGC TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCCCT CGAAGTCCAC CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTTCACAA  
 TGGGACTGCG ACTCGTCTCG TCTGATGCTC TTGTTGTTTC AGATGGGAC GCTTCAGTGG GTAGTCGCCG ACTCGAGGG GCAGTGTTC TCGAAGTGT  
 201 T L T I S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N R  
 ^CDR-L6

701 GGGGAGAGTG TGGTGCCAGC TCCGGTATGG CTGATCCGAA CGGTTCCGC GGTAAAGGACC TGGCATAACT CGAGGCTGAT CCTCTACGCC GGACGCATCG  
 CCCCTCTCAC ACCACGGTCG AGGCCATACC GACTAGGCTT GGCAAAAGGGG CGATTCCTGG ACCGTATTGA GCTCCGACTA GGAGATGGGG CCTGGTAGC  
 235 G E C G A S S G M A D P N R F R G K D L A O  
 ^end of light chain, start of gd tag

801 TGGCCTAGT ACGGAAGTC ACGTAAAGG GGTAACTAGA GGTGAGGTG ATTATGAA AAGAATAATC GCATTCTTC TIGCATCTAT GTTCGTTTT  
 ACCGGGATCA TGGTTCAG TGCATTTC CCAACTGATCT TAAATACTT TTCTCTATAG CGTAAAGAA AACGTAGATA CAAGCAAAA  
 -23  
 ^start of stII

901 TCTATTGCTA CAAACGGTA CGCTGAGGTT CAGCTGGTT AGCTCTGGGG TGGCTGGGG GCTCACTCCG TTTGTCCTGT GCAGCTTCCTG  
 AGATAACGAT GTTGCGCAT GCGACTCAA GTCGACCAAC TCAGACCCG ACCGGACAC GTCGGTCGCC CGAGTGGGC AACAGGACA CGTCGAAGAC  
 -8 S I A T N A Y A E V Q L V E S G G L V Q P G G S L R L S C A A S G  
 ^start of heavy chain

001 GCTTCACCAT TAGTGGTTCT TGGATAACACT GGGTGGTCA GGGCCGGGT AAGGGCTGG ATGGGTTGC TGGATATGGT CCTTATAGGC GCGCTTA  
 CGAAGTGGTA ATCAACAAAGA ACCTATGTCA CCCACGGCACT CCCACGGCACT CCCACGGCACT CCCACGGCACT CCCACGGCACT  
 27 F T I S G S W I H W V R Q A P G K G L E W V A W I A P Y S G A T D  
 ^CDR-H2

101 CTATGCCGAT AGGGTCAAGG GCGCTTAC TATAAGGCA GACACATCA AAAACACAGC CTACCTACAA ATGAAACAGCT TAAGAGCTGA GGACACTGCC  
 GATACGGCTA TCGGAGTCC CGGCAAAGTG ATATTCGCT CTGTGTAGGT TTTTGTGTG GATGGATGTT TACTGTGACT ATTCTGACT CCTGTGACGG  
 60 Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T A  
 ^CDR-H3

201 GTCTTATTGTGGCAAGAGA GGGGGCTTG TACTGGCTGT TCGACTACTG GGCTCAAGGA ACACTAGTC CCGTCTCCCT GGCCTCCACC AAGGGCCAT  
 CAGATAAA CACGGTCTCTT CCGGGGAAAC ATGACCCACA AGCTGATGAC CCCAGTTCTT TGTGATGCTGG CCTGAGGGAG CCCGAGGTGG TTCCCGGGTA  
 93 V Y C A R E G G L Y W V F D Y W G Q G T L V T V S S A S T K G P S  
 ^CDR-H3

301 CGGTCTTCCC CCTGGCACCC TCCTCCAGA GCACCTCTGG GGGCACAGGG GCCCTGGCT GCGCTGGCTT GCGACTACTTC CCCGAACCGG TGACGGTGC  
 GCCAGAAAGGG GGACCGTGGG AGGAGGTCT CGTGGAGACC CCCGGTGTGCC CGGGACCCGA CGGACCACTT CCTGATGAAAG GGGCTTGGCC ACTGCCACAG  
 127 V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P V T V S

FIG. 27B

11401 GTGGAACTCA GGCGCCCTGA CCAGGGCGT GCACACCTTC CCGGCTGTCC TACAGTCTCTC AGGACTCTAC TCCCTCAGCA GCGTGGTGTAC CGTGGCCTCC  
CACCTTGAGT CGCGGGACT GGTCGGCGCA CGTGTGGAA GGCGCACAGG ATGTCAGGAG TCCCTGAATG AGGGAGTGT CGCACCACTG GCACGGGAGG  
160 W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V P S

11501 AGCAGCTTGG GCACCCGAGC CTACATCTGC AACGTGAATC ACAAGCCAG CAAACCCAAG GTCGACAAGA AAGTGTGAAAGC CAAATCTGT GACAAAACTC  
11502 TGTTGAAACC CGTGGGTCTG GATGTAGACG TTGGCACTTAG TGTTGGGTTC CAGCTGTCTC TTCAACTCGG GTTTAGAACACG CTGTTTGAG  
1193 S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K T H

11601 ACCTCAGTGG CGGTGGCTCT GGTTCCGGTG ATTTCGATTA TGAAAGATG GCAAACGCTA ATAAGGGGGC TATGACCGAA AATGCCGATG AAAACGGCT  
TGGAGTCACCCGCCAC TAAAGCCAC TAAAACTAAT ACTTTCTAC CGTTGGAT TATTCCCCG ATACTGGCTT TTACGGCTAC TTTGGCGGA  
227 I S G G S G D F D Y E K M A N K G A M T E N A D E N A L  
End of homology chain

^start of gene III coat protein (267-end)

1701 ACAGCTGAC GCTAAAGGCA AACTTGATTCT TGTCTGCTACT GATTACGGTG CTGCTATCGA TGGTTTCATT GGTGACGTTT CCGGCCTTGC TAATGGTAAT  
TGTCAACTG CGATTTCCGT TTGAACTAAG ACAGGGATGA CTAATGCCAC GACGGATAGCT ACCAAGTAA CCACTGCAA GGCGGAAACG ATTACCCATA  
260 Q S D A K G K L D S V A T D Y G A A I D G F I D V S G L A N G N

11801 GGTGCTACTG GIGATTGTC TGGCTTAAT TCCCAAATGG CTCAGGTGG ATTCACCTT TAATGAATAA TTTCGGTCAA TATTATCCTT  
CCACGATGAC CACTAAAACG ACCGAGATTA AGGGTTAAC GAGTTAGCC ACTGCCACTA TTAAGTGGAA ATTACTTATT AAAGGCAGTT ATAATGGAA  
293 G A T G D F A G S N S Q M A Q V G D G D N S P L M N N F R Q Y L P S

327 L P Q S V E C R P F V F S A G K P Y E F S I D C D K I N L F R G V  
 119901 CCCTCCCTCA ATCGGTGTTGA TGTGCGCCCTT TTGTCCTTTAG CGCTGGTAA CCATATGAAT TTTCTATGA TTGGACAAA ATAAACTTAT TCCGGGTGT  
 GGGAGGAGT TAGCCAAGT ACAGGGAA AACAGAAATC GCGACCAATT GGTACTTA AAAGATAACT AACACTGTT TATTGATAA AGGCACCAACA

360 F A F L L Y V A T F M Y V F S T F A N I L R N K E S O  
 001 CTTTGCCTT CTTTTATATG TTGCCACCTT TATGTATGTA TTTCCTACGT TTGCTAACAT ACTGGCTTAAT AAGGGCTTT AA  
 GAAACGCAA GAAAATATAAC AACGGGGAA ATACATACAT AACGATGTAA TGACGCATTA TTCCCTCAGAA TT

## FIG. - 27C

1 ATGAAAAGA ATATCGCAT TCTTCTTGCA TCTATGTTG TTC TCTTCTAT TGCTACAAAT GCCTATGGAG ATATCCAGAT GACCCAGAT CCGAACGCC  
 1 M K N I A F L I A S M F V F S I A T N A Y A D I Q M T Q S P S S L  
 ^met  
 ^start of signal sequence

101 TGTCCGGCTC TGTGGGCAT AGGGTCACCA TCACCTGCCG TGCCAGTCAG GATGTTCCA CTGCTGTAGC CTGGTATCAA CAGAAACCCAG GAAAGCTCC  
 ACAGGGGAG ACACCCGCTA TCCCAGCTG ACTGGACGCC ACGGTACTGC CTACACAGGT GACCATAGTT GTCTTGGTC CTITTCGAGG  
 35 S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A P  
 ^CDR-L1

201 GAAGGTTCTG ATTACTCGG CATCCCTCCT CTACTCTGG GTCCCTCTC GCTTCTCTGG TAGGGTTCC GGGACGGATT TCACTCTGAC CATCAGCAGT  
 CTTCCGAAGAC TAATGAGGCC GTTAGGAGGA GATGAGACCT CAGGGAAAGAG CGAAGAGACCC ATCGCCAAAGG CCTGCTCAA AGTGTGACTG GTAGTCGTC  
 68 K L I Y S A S F L Y S G V P S R F S G S G T D F T L T I S S  
 ^CDR-L2

301 CTGGCAGCCGG AGACTTCGCC AACTTATTAC TGTAGGCAAC ATTATACTAC TCCTCCACG TTGGACAGG GTACCAAGGT GGAGATCAA CGAACCTGTGG  
 GACGTGGCC TCTGAAGCC TTGAATAATG ACAGTGGTTG TAATATGATG AGGAGGGTGC AAGCCTGTC CATTGGTCCA CCTCTAGTTT GCTTGACACC  
 101 L Q P E D F A T Y Y C Q Q H Y T T P P T F G Q G T K V E I K R T V A  
 ^CDR-L3

35/75

401 CTGCACCCATC TGTCTTCATC TTCCGCCAT CTGATGAGCA GTTGAATCT GGAACCTGCT CTGTTGTG TGCTGTAAT CACTTCTATC CCAGAGGGC  
 GACGTGGTAG ACAGAACTAG AGGGGGTA GACTACTGGT CAACTTGA CCTTGACGG GACAACACAC GGACGACTTA TTGAAGATAG GGTCTCTCG  
 135 A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E A

501 CAAAGTACAG TTGAAGGTGG ATTAACGCCCT COAATCGGGT AACTCCAGG AGAGTGTAC AGCAAGGACA GCACCTACAG CCTCAGCAGC  
 GTTTCATGTC ACCTTCCAC TATTGGGGA GTTGAAGCC TCTCACAGTG TCTCGTCTG TCGTTCCCTGT CGTGGATGTC GGAGTGTGTC  
 168 K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S S

601 ACCCTGACGC TGAGCAAAGC AGACTACGAG AACACACAAAG TCTACGCCG CGAAGTCACC CATCAGGGCC TGAGTCACAAAG AGCTTCACAA  
 TGGGACTGCG ACTCGTTG TCTGTGCTC TTGTGTTAGATGGAC GCTTCAGTGG GTAGTCCCG ACTCGAGCGG GCAGTGTTC TCGAAAGTTG  
 201 T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N R

FIG. 28A

701 GGGGAGGTG TGGGCCAGC TCGGTATGG CTGATCCGAA CGGTAAAGGACC CGGCATAACT CGAGGGCTGAT CCTCTACGCC GGACGCCATCG  
CCCCTCTCAC ACCACGGTCG AGGCCATACC GACTAGGCTT GGCAAAAGGG CCATCCTGG ACCGTATTGA GCTCCGACTA GGAGATGGGG CCTGGTAGC  
235 G E C G A S S G M A D P N R F R G K D L A O

^end of light chain, start of gd tag

801 TGGCCCTAGT ACGCAAGTC ACGTAAAGG GGTAACTAGA GGTGAGGTG ATTATGAA AAAGAATATC GCATTCTTC TGCCATCTAT GTTCGTTTT  
ACCGGGATCA TGGCTCAAG TGCATTTC CCAACTGATCT CAAACTAAC TAAATACTT TTCTCTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAA  
-23

^start of stII

901 TCTATTGCTA CAAACGGTA CGCTGAGGT CAGCTGGTGG AGTCTGGGG TGGCTGGTG CAGCCAGGG GCTCACTCCG TTGTCCTGT GCAGCTCTG  
AGATAACGAT GTTGCAT GCGACTCAA GTCGACCC ACCGGACCAAC GTCGGTCCCC CGAGTGGGC AACAGGACA CGTCGAAGAC  
-8 S I A T N A Y A E V Q L V E S G G G L V Q P G G S L R L S C A A S G  
^start of heavy chain

36/75 101 GCTTCACCAT TAGTAATTAT GGGATAACACT GGGTGGCTA GGCCCCGGGT AATGGGGTGG TAGGATTCTT CCTCTCTAACG GCTCTACTTA  
CGAAGTGGTA ATCTTAATA CCCTATGTA CCCATGCA CCCACGGCACT CCGGGGCCCA TTCCGGGACC TTACCCAAAC ATCCTAAGA GGAAGATTGC CGAGATGAAT  
27 F T I S N Y G I H W V R Q A P G K G L E W V G R I S P S N G S T Y  
^CDR-H2

36/75

101 CTATGCCGAT AGGGTCAAGG GCCGTTTAC TATAAGGCCA GACACATCA AAAACACAGC CTACCTCAA ATGAAACAGCT TAAGAGCTGA GGACACTGCC  
GATAACGGCTA TCGGAGTTCC CGGGAAAGTG ATATCGCGT CTGTTAGGT TTTTGTGTCG GATGGATGTT TACTTGTGCA ATTCTCGACT CCTGTGACGG  
60 Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T A

201 GTCTTATTAT GTGCAAATG CTCGGTCAAGG TTCGGTTACT GGGGTCAGG AACACTAGTC ACCGCTCTCC CGGGCCCTCCAC CAAGGGCCA TCGGTCTTCC  
CAGATAATA CACGTTTAC GAGCCAGTCC AAGGAAATGA CCCCAGTTC TGTGATCAG TGGCAGAGGA GCGGGAAGGT GTTCCGGGT AGCCAGAAGG  
93 V Y Y C A K C S V R F A Y W G Q G T L V T V S S A S T K G P S V F P  
^CDR-H3

FIG. 28/6

101 CCCTGGCACC CTCCCTCCAAG AGCACCTCTG GGGCACAGC GCCCCCTGGC TGCCTGGCTCA AGGACTACTT CCCCGAACCG GTGACGGTGT CGTGGAACTC  
 27 L A P S S K S T S G G T A A L G C L V K D Y F P E P V T V S W N S

01 AGGGCCGCGT ACCAGGGGG TGGCACACCTT CCCGGCTGTC CTACAGTCTT CAGGACTCTA CTCCCTCGC AGGACCAAGT TCCCTGATGAA GGGGCTGGC CACTGCGACA GCACCTTGAG  
 60 G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V P S S S L

01 GGCACCCAGA CCTACATCTG CAACTGTAAAT CACAAGCCA GCACACCAA GGTCGACAAG AAAGTGTAGC CCAAATCTTG TGACAAACT CACCTCAGTGC  
 37 CCGTGGGTCT GGATGAGC GTTGCACCTA GTGTTGGGT CGTGTGGTT CCAGCTGTC TTTCACACTCG GGTTAGAAC ACTGTTGA GTGGAGTCAC  
 93 G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K T H L S G

^end of heavy chain  
start of gene III coat protein (267-end) ^

01 GGGTGGCTC TGGTTCGGT GATTTGATT ATGAAAAGAT GGCACAAACGGT AATAAGGGG CTATGACCGA AAATGCCAT GAAACCCAT TACAGTCTGA  
 37 CGCCACCGAG ACCAAGGCCA CTAAGACTAA TACTTTCTA CGGTTGCGA TTATTCCCC GATACTGGCT TTACGGCTA CTTTGGCG ATGTAGACT  
 60 A K G K I D S V A T D Y G A A I D G F I G D V S G L A N G N G A T

01 CGCTAAAGGC AAACTGATT CTGTCGCTAC TGAATTACGGT GCTGCTATCG ATGGTTCAT TGGTGACGT TCCGGCCTTG CTAATGGTAA TGGTGACT  
 37 CCGATTTCGG TTGGAACCTAA GACAGGGATG ACTTAATGCCA CGACGGATAGC TACCAAAAGTA ACCACTGCAA AGGGCGAAC GATTACATT ACCACGATGA  
 60 A K G K I D S V A T D Y G A A I D G F I G D V S G L A N G N G A T

01 GGTGATTGT CTGGCTCTAA TCCCCTAAATG GCTCAAGTCG GTGACGGTGA TAATTCACT TTAATGAATA ATTTCGCTCA ATATTTACCT TCCCTCCCTC  
 37 CCACTAAAC GACCGAGATT AAGGGTTAC CGACTGCTAGC CACTGCCACT ATTAAAGTGGAA AATTACTTAAAGGCGT TATAATGGA AGGGGGAG  
 93 G D F A G S N S Q M A Q V G D G D N S P L M N F R Q Y L P S I P Q

01 ATCGGGTGA ATGTCGCCCT TTGTCCTTA GCGCTGGTAA ACCATATGAA TTTTCATG ATTGTGACAA AATAAACTTA TTCCGTGGT TCTTTCGTT  
 27 TAGCCAACT TAGACGGGA AACAGAAAT CGCGACCAATT TGTGTACTT AAAAGATAAC TAACACTGTT TTAATTTGAAT AAGGCACAC AGAACGCAA  
 60 S V E C R P F V F S A G K P Y E F S I D C D K I N L F R G V F A F

01 TCTTTTATAT GTTGCACCT TTATGTATGT ATTTCCTACG TTTCCTAACAA TACTGGTAA TAAGGAGTCT TAA  
 AGAAAATATA CAACGGTGGAA AACACATAACA TAAAAGATGC AAACGATGT ATTCCCTCAGA ATT  
 60 L L Y V A T F M Y V F S T F A N I L R N K E S O

FIG. - 28 C

1 ATGAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTCTAT TGCTACAAAT GCCTATGCCAT CCGATATCCA GATGACCCAG TCCCCGAGCT  
 TACTTTCT TATAGCTAA AGAAGAACGT AGATACAGG AAAAAGATA ACCGATGTTA CGGATACGTA GGCTATAGGT CTACTGGCTC AGGGGCTCGA  
 1 M K K N I A F L L A S M F V F S I A T N A Y A S D I Q M T Q S P S S  
 ^met ^start of stII signal sequence

101 CCCTGTCCGC CTCTGGGGC GATAGGGTCA CACACCTG CCGTGCAGT CAGGATGTGT CCACTGGCTG AGCCTGGTAT CAACAGAAC CAGGAAAGC  
 GGGACAGGGG GAGACACCG CTATCCAGT GTAGTGGAC GGCACGGTC GTCCTACACA GGTGACGACA TGGACCATA GTTGTCTTGT GTCCTTTCG  
 35 I S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A  
 ^CDR-L1

201 TCCGAAGCTT CTGATTACT CGGCATCCCTT CCTCTACTCT GGAGTCCCTT CTGGCTCTC TGGTAGGGT TCCGGACGG ATTCTACTCT GACCATCAGC  
 AGGGCTTCGAA GACTAAATGA GCGGTAGGAA GGAGATGAGA CCTCAGGGAA GAGGAAAGAG ACCATGCCA AGGCCCTGCC TAAAGTGAGA CTGGTAGTCG  
 68 P K L I I Y S A S F L Y S G V P S R F S G S G T D F T I T I S  
 ^CDR-L2

301 AGTCGCAGC CGGAAGACTT CGCAACTTAT TACTGTCAAGC AATCTTATAC TACTCTCTCCC ACGTTCCTCCC AGGGTACAA GGTGGAGTC AAACGAACG  
TCAGACGTG GCCTTCTGAA GCGGTAGGAA ATGACAGTAGC TTAGAAATAG ATGAGGAGGG TGCAAGGCTG TCCCATGGTT CCACCTCTAG TTGGCTTGAC  
 101 S I Q P E D F A T Y Y C Q Q S Y T T P P T F G Q G T K V E I K R T V  
 ^CDR-L3

401 TGGCTGCACC ATCTGTCTTC ATCTTCCGC CATCTGATGA GCAGTTGAAA TCTGGAACGT CCTCTGTGT GTGCCCTGCTG AATAACTCT ATCCAGAGA  
 ACCGACGTGG TAGACAGAAG TAGAAGGGCG GTAGACTACT CGTCAACTTT AGACCTTGAC GGAGACAAACAA CACGGACGAC TTATTGAGA TAGGGCTCT  
 135 A A P S V F I F P P S D E Q I K S G T A S V V C L L N N F Y P R E

501 GGCCAAAGTA CAGTGGAAAGG TGGATAACGC CCTCCAATCG GGTAAACTCCC AGGGAGACTGT CACAGAGC GACAGCAAGG ACAGCACCTA CAGCCCTCAGC  
 CCGGTTTCAT GTCACCTTC ACCTATGGCG GGAGGTTAGC CCATTGAGG TCCTCTCACA GTGTCTGTC CTGTGTTCC TGTCTGGAT GTCGGAGTCG  
 168 A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S I S

601 AGCACCTGAA CGCTGAGCA AGCAGACTAC GAGAAACACA AAGTCTACGC CTGGAAAGTC ACCCATCAGG GCCTGAGCTC GCCGTGTCACAA AAGAGCTTC  
 TCGTGGACT GCGACTCTCGT TCGTCTGATG CTCTTGTGT TTCAAGATGCG GACGCTTCAG TGGGTAGTCC CGGACTCGAG CGGGCAGTGT TTCTGAGT  
 201 S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N

1) ACAGGGGAGA GTGTGGGCC AGCTCCGGTA TGGCTGATCC GAACCGTTTCC CGGGTAAAGG ACCTGGCATA ACTCGAGGT GATCCTCTAC GCCGGACGCA  
 15 R G E C G A S S G M A D P N R F R G K D L A O  
 ^end of light chain, start of gd tag

1) TCGGGCCCT AGTACGCAAG TTCACGTAAA AAGGGTAACT AGAGGTGAG GTGATTAT GAAAAGAAT ATCGCATTC TTCTGGCATC TATGTTGCGTT  
 AGCACGGGA TCATGGTTC AAGTGCATT TTCCCAATTGA TCTCCAACTC CACTAAAATA CTTTCTTA TAGCGTAAG AAGAACGTAG ATACAAGCAA  
 13 M K K N I A F L L A S M F V  
 ^start of stII

1) TTTTATTCG CTACAAACGC GTACGGCTGAG GTTCAGCTGG TGAGGTCTGG CGGTGGCTG GTGCGCCAG GGGGCTCACT CGGTGTCGC TGTGCGACT  
 AAAAGATAC GATGTTGCG CATGGCAGTC CAAGTGCACC ACTCTAGACC GCCACCGGAC CACTCGCTC CCCCCAGTGA GGCACACAGG ACACGTCGAA  
 9 F S I A T N A Y A E V L V Q P G S L R L S C A A S  
 ^start of heavy chain

1) CTGGCTTCAC CATTAGTGGT TCTGATATAC ACTGGGTGG TCAGGGCCCG GGTAGGGCC TGGATGGGT TGGTAGGATT TCTCTTATG GGGCAATAC  
 39/6 G F T I S G S D I H W V R Q A P G K L E W V G R I S P Y G G N T  
 ^start of heavy chain

1) TAACTATGCC GATAAGGTCA AGGGCCGTT CACTATAAGC GCAGACACAT CCAAAACAC AGCCTACCA CAAATGAACA GCTTAAGAGGC TGAGGACACT  
 ATTGATACGG CTATGCCAGT TCCCGGGCAA GTGATATTGCG CGTCTGTGTA GGTTTGTGTTG TCGGATGGAT GTTGTACTGT CGAATTCTCG ACTCTCTGTGA  
 19 N Y A D S V K G R F T I S A D T S K N T A V L Q M N S L R A E D T

1) GCGGTCTATT ATTGTCGAAG AGTCCGGCCG CTCAGGTGCG TGTTCGACTA CTGGGGCTCAA GGAAACACTAG TCACCGTCTC CTGGCCTCC ACCAAGGGCC  
 39/5 CCCAGATTA TAACAGGTTC TCAAGCTGAG GAGTTCAGC ACAAGCTGAT GACCCAGT CCTGTGATC AGTGGCAAG GAGCCGGAGG TGGTTCCGG  
 12 A V Y Y C A R V G G L K L F D Y W G Q G T L V T V S S A S T K G P  
 ^CDR-H3

1) CATGGGTCTT CCCCCGGCA CCTCTCTCCA AGGACCCCTC TGGGGCACA GGGCCCTGG GCTGGCTGGT CAAGGACTAC TTCCCGAAC CGGTGACGGT  
 GTAGCCAGAA GGGGACCGT GGAGGGAGGT TCTCGTGGAG ACCCCCGTGT CGACGGACCA GTTCCTGATG AAGGGCTTG GCCACTGCGCA  
 6 S V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P V T V

FIG. 29B

1401 GTCGTGGAAC TAGGGCCCC TGACCAAGACC CGTGCACACC TTCCCCGGCTG TCCTAGACTC CTCAGGACTC TACTCCCTCA GCAGCGTGGT GACCGTGGCC  
 159 S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V P

1501 TCCAGGAGCT TGGGACCCCA GACCTAACATC TCGAACGTGA ATCACAAGCC CAGAACACC AAGGTCGACA AGAAAGTGA GCCCAAATCT TGTGACAAA  
 AGGTGCTCGA ACCCGTGGGT CTGGATGGACT ACGTGGTAG ACGTGGACT TAGTGTCTGG GTCTGGTGG TTCCAGGTGT TCTTCAACT CGGGTTAGA ACACTGTTT  
 192 S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K T  
 ^end of heavy chain, start of leucine zipper

1601 CTCACGGCCG CATGAAACAG CTAGAGGACA AGGTGGAAGA GCTACTCTCC AAGAACTACC ACCTAGAGAA TGAAGTGGCA AGACTCAAAA AACTGTCGG  
 GAGTGGGGC GIACTTGTG GATCTCTGT TCAAGCTCTCGT CGATGAGGAGG TTCTGTGATGG TGGATCTCTT ACTTCACCGT TCTGAGTTT TTGAAACAGCC  
 226 H G R M K Q L E D K V E L I S K N Y H L E N E V A R L K K L V G

1701 GGAGGCCGGA AAGCTTAGTG GCGGTGGCTC TGGTTCGGT GATTTTGATT ATGAAAAGAT GGAAACGCT AATAAGGGG CTATGACCGA AAATGCCGAT  
 CCTCGGCCCT TTGAAATCAC CGCCACCGAG ACCAAGGCCA CTAAGCTAA TACTTTCTCA CGGTGCTGGCA TTATCCCC GATACTGGCT TTACGGCTA  
 259 E R G K L S G G S G D F D Y E K M A N A N K G A M T E N A D  
 ^end of leucine zipper, gene III coat protein (267-end)

1801 GAAACGGCG TACAGTCTGA CGCTAAAGGC AACTTGATT CTGTCGGCTAC TGATTACGGT GCTGCTTACG ATGGTTTCAT TGCTGACGGT TCCGGCTTG  
 CTTTGCGCG ATGTCAGACT GCGATTTCGG TTGAACTAA GACAGCGATG ACTAATGCCA CGACGATAGC TACCAAAGTA ACCACTGCCA AGGCCGGAAC  
 292 E N A L Q S D A K G K L D S V A T D Y G A A I D G F I G D V S G L A

1901 CTAATGGTAA TGGTGTACT GGTGATTCTG CTGGCTCTAA TTCCCCAATG GCTCAAGTGC GTGACGGTGA TAATCACCT TAAATGAATA ATTCGGTCA  
 GATTACCATTAACACGATGA CCACTAAAC GACCGAGATT AAGGGTTTAC CGAGTTCAAGC CACTGGCACT ATTAAGTGGAA ATTACTTAT TAAAGGCACT  
 326 N G N G A T G D F A G S N S Q M A Q V G D G D N S P L M N N F R Q

40/75

1901 CTAATGGTAA TGGTGTACT GGTGATTCTG CTGGCTCTAA TTCCCCAATG GCTCAAGTGC GTGACGGTGA TAATCACCT TAAATGAATA ATTCGGTCA  
 GATTACCATTAACACGATGA CCACTAAAC GACCGAGATT AAGGGTTTAC CGAGTTCAAGC CACTGGCACT ATTAAGTGGAA ATTACTTAT TAAAGGCACT  
 326 N G N G A T G D F A G S N S Q M A Q V G D G D N S P L M N N F R Q

2001 ATATTTACCT TCCCTCCCT AATCGGTGA ATGTCGGCTTAA GCGCTGGTAA ACCATATGAA TTTTCTATG ATTTGACCAA AATAAACTTA  
 TATAATGGAA AGGGAGGGAG TTAGGCAACT TACAGCGGGGA AAAAGATAAC CGCACCATT TGGTATACTT AAAAGATAAC TAAACACTGGT TTATTGAAAT  
 359 Y L P S L P Q S V E C R P F V F S A G K P Y E F S I D C D K I N L

2101 TTCCGGGGTG TCTTTGGCTT TCTTTGCTACT ATTTCTACG TTGCTAACAA TACTGGTAA TAAGGAGTCT TAA  
 AAGGCACCAAGAACGCCAA AGAAACGCCAA AGAAAATATA CAACGGTGGAA AATACATACA TAAAGATGC AAACGATTTGT ATGAGCCTATT ATTCCCTCAGA ATT

392 F R G V F A F L I Y V A T F M Y V F S T F A N I L R N K E S O

FIG. 29 C

1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTCTAT TGCTACAAAT GCCTATGCCAT CGGATATCCA GATGACCCAG TCCCGAGCT  
 TACTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAACAGATA AGCATGTTA CGGATACGTA GGCTATAGGT CTACTGGTC AGGGCTCGA  
 1 M K K N I A F L L A S M F V F S I A T N A Y A S D I Q M T Q S P S S  
 ^start of still signal sequence  
 ^met

101 CCCCTGCGC CTCGTGGC GATAGGGTCA CCATCACCTG CCGTGCCAGT CAGGATGTGT CCACTGCTGT AGCTGGTAT CAACAGAAC CAGGAAAGC  
 GGGACAGGGC GAGACACCCG CTATCCAGT GGTAGTGGAC GGGACGGTC GTCCTACACA GGTCACGACA TCGGACATA GTGCTCTTTCG  
 35 L S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A  
 ^met

201 TCCGAAAGCTT CTGATTACT CGGCATCCTT CCTCTACTCT GGAGTCCCTT CTCGCTTCTC TGGTAGGGT TCCGGACGG ATTCACTCT GACCATCAGC  
 AGGCTTCGAA GACTAAATGA GCGCTAGGAA GGAGATGAGA CCTCAGGGAA GAGCGAAGAG ACCATGCCA AGGGCTGTC TAAAGTGAGA CTGGTAGTCG  
 68 P K L L I Y S A S F L Y S G V P S R F S G S G T D F T L T I S  
 ^CDR-L2

301 AGTCTGCAGC CGGAAGACTT CGCAACTTAT TACTGTCAG AACTTATAC TACTCTCCC ACGTTCGGAC AGGGTACCA GGTTGGAGTC AATAACTCT ATCCAGAGA  
 TCAGACGTCG GCCTTCTGAA GGCTTGAATA ATGACAGTCG TTGAAATATG ATGAGGGAGG TGCAAGGCTG TCCCATGGT CCACCTCTAG TTTGGCTTGAC  
 101 S L Q P E D F A T Y Y C Q Q S Y T T P P T F G Q G T K V E I K R T V  
 ^CDR-L3

41/75

401 TGGCTGCACC ATCTGTCTTC ATCTTCCGC CATCTGATGAA GCAGTTGAAA TCTGGAAACTG CCTCTGTGT GTGCCCTGCTG AATAACTCT ATCCAGAGA  
 ACCGACGTCG TAGACAGAA TAGIAGGGGG GTAGACTACT CGTACACTT AGACACTT AGTCACACTT AGACCTCTGAC GGAGACAAACA CACGGACGAC TTATTGAGA TAGGGTCTCT  
 135 A A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E

501 GGCCAAAGTA CACTGGAAAGG TGGATTAACGC CCTCCAACTG GGTAACTCCC AGGAGAGTGT CACAGGGAG GACAGAACCTA CACGGACCTA CAGCCCTAGC  
 CCGGTCTCAT GTCACCTTC ACCTATTGCG GGAGGTTAGC CCATTGAGGG TCCTCTCACA GTGTCCTCGTC CTGTCGTTCC TGTCTGGAT GTCGGAGTCG  
 168 A K V Q W K V D N A I Q S G N S Q E S V T E Q D S K D S T Y S L S

601 AGCACCCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC CTGCGAAGTC ACCCATCAGG GCCTGAGTC GCCTGTCACA AAGAGCTCA  
 TCGTGGGACT GCGACTCTCGT TCGTCTGATG CTCTTGTGT TCGAGATGCG GACGCTTCAG TGGTAGTCAG CGGACTCGAG CGGGCAGTGT TTCTCGAAGT  
 201 S T I T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N

FIG. 30A

701 ACAGGGGAGA GTGGGGTGC AGCTCCGGTA TGGCTGATCC GAACCGTTTC CGGGTAAGG ACCTGGCAT AACTGAGGGT GATCCTCTAC GCGGGACGCA  
TGTCCCTCT CACACCACGG TCGAGGCCAT ACCGACTAGG CTTGGCAAAG GCGCCATTCC TGGACCGTAT TGACCTCCGA CTAGGAGATG CGGCCCTGCGT  
135 R G E C G A S S G M A D P N R F R G K D L A O  
^end of light chain, start of gd tag

101 TCGTGGCCCT AGTAGCAAG TTCACGTAAG AAGGGTAACT AGAGGGTGGAG GTGATTTAT GAAAAGAAAT ATCGCATTTC TTCTTGATC TATGTTCTGT  
AGCACCGGGA TCATGGTTC AAGTGCATT TTCCCATG AACTCCAACTC CACTAAATAA CTTTTCTTA TAGCCTAAAG AAGAACGTAG ATACAACCAA  
23 M K K N I A F L L A S M F V  
^start of stII

01 TTTCTATG CTACAAACGC GTACGCTGAG GTTCAGCTGG TGGAGTCTGG CGGTGGCCCTG GTGAGGCCAG GGGGCTACT CGGGCTATC TGTGAGCTT  
AAAAGATAAC GATGTTGCG CATGGGACTC CAAGTCGACC ACCTCAGACC GCAACGGAC CACGTCGGTC CCATTCGGG ACCTTACCCA ACGATGATAA ATAGGAATAAC CGCCGATATG  
-9 F S I A T N A Y A E V Q L V E S G G L V Q P G G S L R L S C A A S  
^start of heavy chain  
42/75  
01 CTGGCTTCAC CATTACTAAT TCCGATATAC ACTGGGTGGC TCAAGGGCCG GGTAAAGGGCC TGGAATGGGT TGCTACTATT TATCCTTATG GCGGCTATAC  
GACCGAAGTG GTAATGATTA AGGCTATATG TGACCCACGC ACTTCGGGC ACTTCGGG ACCTTACCCA ACGATGATAA ATAGGAATAAC CGCCGATATG  
6 G F T I T N S D I H W V R Q A P G K G L E W V A T I Y P Y G G Y T  
^start of heavy chain  
^CDR-H1

01 TACTATGCC GATAGGTCA AGGGCGTT CACTATAAGC GCAGACACAT CCAAAACAC AGOCTACCTA CAAATGACA GCTTAAGAGGC TGAGGACACT  
AATGATAACGG CTATGGCAGT TCCCGGCAA GTGATATTG CGTCTGTGTA GGTTTTGTG TCGGATGGAT GTTACTGTG CGATTCTCG ACTCCTGTGA  
9 Y Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T  
^CDR-H2

01 TACTATGCC GATAGGTCA AGGGCGTT CACTATAAGC GCAGACACAT CCAAAACAC AGOCTACCTA CAAATGACA GCTTAAGAGGC TGAGGACACT  
AATGATAACGG CTATGGCAGT TCCCGGCAA GTGATATTG CGTCTGTGTA GGTTTTGTG TCGGATGGAT GTTACTGTG CGATTCTCG ACTCCTGTGA  
1 GCGGTCTAT ATTGGCAAG AGGGGGGG ATGGACGGGT ACGTATGGG CTACTGGGGT CAAGGAACAC TAGTCACCGT CTCCCTGGCC TCCACCAAGG  
CGGCAGATAA TAACACGTT TCCCGGGCC TACCTGGCGA TGCAATAACCT GATGACCCA GTTCTTGTG ATCAAGTGGCA GAGGAGCCGG AGGTGGTCC  
2 A V Y Y C A R G G M D G Y V M D Y W G Q G T L V T V S S A S T K G  
^CDR-H3

1 GCGCATGGT CTTCCCCCTG GACCCCTCCT CCAAGAGGCAC CTCTGGGGG ACAGGGGGC TGGGCTGCCT GGTCAGGAC TACTTCCCCG AACGGGTGAC  
CGGGTAGCCA GAAGGGGGAC CGTGGGAGGA GGTTCTCGTG GAGACCCCCG TGTGGGGG ACCCGACGGA CCAGTTCTG ATGAAGGGC TTGGCCACTG  
6 P S V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P V T

FIG.- 30/8

1401 GGTGTCGTTG AACTCAGGG CCGTGACCA CGGGTGGCAC ACCTTCCGG CTGTCCTACA GTCCCTCGG CTCTACTCCC TCAGGAGGT GGTGACCGT GGCACAGGCAC CCACAGGCACC TTGAGTCCGC GGGACTGGTC GCGGCACGTC TGGAGGGCC GACAGGTGT CAGGAGTCT GAGATGAGGG AGTCGTGCGA CCACTGGCAC  
 159 V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V  
 1501 CCCTCAGCA GCTTGGCAC CCAGACTAC ATCTGCAAC TGAAATCACAA GCCAGCAAC ACCAAGGTG ACAAGAAAGT TGAGCCCAA TCTTGTGACA GGGAGGTGCGT CGAACCCTG GGTCTGGAT TAGACGTTGC ACTTAGTGT TGTTCTCGT TGTTCCAGC TGTTCTGAGT ACTCGGGTT AGAACACTGT  
 192 P S S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K  
 1601 AAACTACGG CGGCATGAA CAGCTAGGG ACAGGGTCAA AGAGCTACTC TCCAGAAACT ACCACCTAGA GAATGAAGTG GCAAGACTCA AAAACTGTGT  
 226 T H G R M K Q L E D K V E E L L S K N Y H L E N E V A R L K K L V  
 ^end of heavy chain, start of leucine zipper

1701 CGGGAGGGC GAAAGCTTA GTGGCATGTTCC GGTGATTGG ATTATGAAAA GATGGCAAAAC GCTATAAAGG GGGCTATGAC CGAAATGCC  
 GCCCCTGGG CCTTTCGAAT CACCGCACC GAGCAAGG CCACTAAAC TAATACCTTT CTACCGTTTG CGATATTCC CGGATACTG GCTTTACGG  
 259 G E R G K L S G G S G D F D Y E K M A N K G A M T E N A  
 ^end of leucine zipper, start of gene III coat protein (267-end)

.801 GATGAAACG CGCTACAGTC TGACGCTAA GGCAAACTG ATTCTGTCGC TACTGATTAC GGTGCTGCTA TCGATGGTT CATGGTGCAC GTTTCCGGCC  
 CTACTTTGCG GCGATGTCAG ACTGCGATT CCGGTGTGAAAC TAAGACAGCG ATGACTAATG CCACGACGAT AGCTACCAA GTAACCACTG CAAAGGCCGG  
 292 D E N A L Q S D A K G K L D S V A T D Y G A A I D G F I G D V S G L

1901 TTGCTAATGG TAATGGTGTACTGGTGTGTTGCTC TAATTCCAA ATGGCTCAAG TCGGTGACGG TGATTAATGA CCTTTAATGA ATATAFTCCG  
 AACGATTACCA ATTACACCA TGACCACTAA AACGACCGAG ATTAAAGGGTT TACCGAGTTC AGCCACTGGCC ACTATTAAGT GAAATTACT TATTAAGGC  
 326 A N G N G A T G D F A G S N S Q M A Q V G D N G D N S P L M N N F R

2001 TCAATATTA CCTTCCCTCC CTCAATGGT TGATGTCGC CCTTFTGCTT TTAGGGCTG TAACCATTAT GAATTCTA TTGATTTGCA CAAATAAAC  
 AGTTATAAT GGAAGGGAGG GAGTTAGCCA ACTTACAGCG AACAGGGTGGTAAATGGTATA CTAAAAGAT AACTAACACT GTTTTATTTG  
 359 Q Y L P S L P Q S V E C R P F V F S A G K P Y E F S I D C D K I N

2101 TTATTCCGTG GTGGCTTTCG GTTCTTCTTA TATGTTGCCA CCTTATGTA TGTATTTCT ACATACTGGC TAATAGGAG TCTTAA  
 AATAAGGCAC CACAGAAACG CAAAGAAAT ATACAACGGT GGAAATACAT ACATAAAAGA TGCAAAACGAT TGTATGACGC ATATTCCCTC AGAATT  
 392 L F R G V F A F L L Y V A T F M Y V F S T F A N I L R N K E S O

1 ATGAAAAGA ATATCGCAT TCTTCTTGCA TCTATGCTTCTAT TGGTACAAAT GCGTATGCCAT CGGATATCCA GATGACCCAG TCCCCGAGCT  
 1 TACTTCTTCTATAGTAGGTAAAGGATACAGT AGGATACAAGC AAAAAGATA ACCATGGTTA CGGATACTGA GGCTATAGGT CTACTGGTC AGGGGCTCGA  
 1 M K N I A F L I A S M F V F S I A T N A Y A S D I Q M T Q S P S S  
 ^met ^light chain start

101 CCCTGCCGC CTCTGTGGC GATAAGGTCA CCATCACCTG CCGTGCAGT CAGGATGTGT CCACTGCTGT AGCCTGGTAT CAACAGAAC CAGGAAAGC  
 GGGACAGGGC GAGACACCCG CTATCCAGT GTTAGTGGAC GGCACGGTCA GTCCTACACA GGTGACGACA TCGGACCCATA GTCTGTCTTG GTCCCTTTTCG  
 35 L S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A  
 ^CDR-L1

201 TCCGAAGCTT CTGATTTACT CGGCATCCCTT CCTCTACTCT GGAGTCCCTT CTCGCTTCTC TGGTAGGGT TCCGGGACGG ATTTCACTCT GACCATCAGC  
 AGGCTTCGAA GIACTAAATGAA GCGGTAGGAA GGAGATGAGA CCTCAGGGAA GACCGAAGAG ACCATCGCCA AGGGCTGCC TAAAGTGAGA CTGGTAGTCG  
 68 P K L I Y S A S F I Y S G V P S R F S G S G S G T D F T I T I S  
 ^CDR-L2

301 AGTCCTGCAGC CGGAAGACTT CGCAACTTAT TACTGTGAGC AATCTTATAC TACTCTCC ACGTTCGGAC AGGGTACCAA GGTTGGAGTC AAACGAAGCTG  
 TCAGACGTG GCCTTCTGAA GCGGTAGAAG TAGAAGGGGG GTAGACTACT CGTCAACTT AGACAGTCG TTAGAATATG ATGAGGGGG TGCAAGCCTG TCCCATGGTT CCACCTCTAG TTGCTTGAC  
 101 S L Q P E D F A T Y Y C Q Q S Y T T P P T F G Q G T K V E I K R T V  
 ^CDR-L3

44/75

401 TGGCTGCACC ATCTGTCTTC ATCTTCCGC CACTGTGATGA GGAGTTGAAA TCTGGAACTG CCTCTGTGT GTGCTCTG ATAAACTCT ATCCCAGAGA  
 ACCGACGTGG TAGACAGAAAG TAGAAGGGGG GTAGACTACT CGTCAACTT AGACAGTCG TTAGAATATG ATGAGGGGG TGCAAGCCTG TCCCATGGTT CCACCTCTAG TTGCTTGAC  
 135 A A P S V F I F P P S D E Q L R S G T A S V V C L L N N F Y P R E

501 GGCCAAAGTA CAGTCGAAGC TGGATAACGC CCTCCCAATCG GGTAACTCCC AGGAGACTGT CACAGGGAG CACGCCAGT CAGGCCCTA CAGCCCTAGC  
 CCGGTTCAT GTCACCTTCC ACCTATGCG GGAGGGTAGC CCATTGGGG TCCTCTCACA GTGTCTCGTC CTGTCGTGGAT GTCGGAGTCG  
 168 A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S

601 AGCACCCCTGA CGCTGAGCAA AGCAGACTAC GAGAAAACACA AAGTCTACGC CTGCGAAGTC ACCCATCAGG GCCTGAGCTC GCCCCTCACCA AAGAGCTTC  
 TCGTGGGACT GCGACTCTCGTT TCGTCTGATG CTCTTGTGT TTCAGATGCG GACGCTTCAG TGGTAGTCC CGGACTCGAG CGGGCAGTGT TTCTCGAAGT  
 201 S T L T I S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N

FIG.- 314

11 ACAGGGGAGA GTGTGGTGC CAGCTCCGGTA TGGCTGATCC GAACTGGTAAAGG ACCTGGCAT AACTCGAGGT GATCCTCTAC GCGGGACGCA  
 15 TGTCCCCCT CACACACGG TCGAGGCCAT ACCGACTAGG CTGGCCAAAG GGGCCATTCC TGGACCGTAT TGAGGCTCGA CTAGGAGATG CGGCCTGCGT  
 15 R G E C G A S S G M A D P N R F R G K D L A O  
 ^ end of light chain, start of gd tag

11 TCGTGGCCT AGTACGCAAG TTCACGTAA AAGGGTAAC AGAGGGTAAC AGAGGGT GAG GTGATTATG GAAAAGAAT ATCGCATTC TTCTTGCAATC TATGTTCGTT  
 15 AGCACCGGGA TCATGGTTC AAGTGGATT TTGGCATTT TCTCCAACTC CACTAAATA CTTTTCTTA TAGGGTAAG AAGAACGTTAG ATACAAGCAA  
 15 M K K N I A F L I A S M F V

13 ^start of stII

1 TTTTCATG CTACAAACGC GTACGGTGA GTTACGGTGG TGGAGTCTGG CGGTGGCTTG GTGAGGCCAG GGGGCTCACT CCGTTTGTC CCGTTTGTC CTTGAGCTT  
 15 AAAAGATAAC GATGTTGCG CATGGCACTC CAAGTGGACC ACCTCGAACCC GCAACGGAC CACGTGGTC CCCCCAGTGA GGCAAAACAGG ACACGTCGAA  
 15 9 F S I A T N A Y A E V Q L V E S G G L V Q P G G S L R L S C A . A S  
 ^start of heavy chain

1 CTTGGCTTCAC CATTAAATATC ACTGATATAAC ACTGGCTGG TCAGGGCCCG GGTAAAGGCC TGGAATGGGT TGGTTATATT TCTCTCCTTA GCGGGCGCTAC  
 15 GACCGAAGTG GAAATTATTA ATACTATATG TGACCCACGG AGCTCGAACCC CCATTGGGG ACCTTACCCA ACCAATATAA AGAGGAGGAT CGCCGGGATG  
 15 9 F T I N N Y D I H W V R Q A P G K G L E W V G Y I S P P S G A T  
 ^CDR-H2

1 TTACTATGCC GATAAGCTCA AGGGCCGT CACTATAAGC GCAGACACAT CCAAAACAC AGCCTACCA CAAATGACA GCTTAAGAGC TGAGGACACT  
 15 AATGATAACGG CTATGCCAGT TCCGGCAAAT GTGATATTG CGTCTGTGTA GGTGTTTG TGCGATGGAT GTTACTTGT CGAAATTCTCG ACTCTGTGA  
 15 9 Y Y A D S V K G R F T I S A D T S K N T A Y I Q M N S L R A E D T

1 GCGGTCTAT ATTGGCAAG AATGGTCGG ATGGGGGG GGGTTATGGA CTACTGGGT CAAGGAACAC TAGTCACCT CTCCCTGGCC TCCACCAAGG  
 15 45/75 CGGGCAGATAA TAACACGGTC TTACCAAGCCC TACGGCTCCC CCCAAATACCT GATGACCCCA GTTCTTGTG ATCAAGTGGCA GAGGAGCCGG AGGTGGTTCG  
 15 2 A V Y Y C A R M V G M R R G V M D Y W G Q G T L V T V S S A S T K G  
 ^CDR-H3

1 GCCCCATCGGT CTTCCCTG GCACCCCT CCAAGAGGCAC CTCTGGGG ACAGGGCCC TGGGCTGGCT GGTCAAGGAC TACTTCCCCG ACCGGTGA  
 15 CGGGTAGCCA GAAGGGGGAC CGTGGGAGGA GGTTCTCGTG GAGACCCCG TGTGCGGGG ACCCGACGGA CCAGTTCTG ATGAAAGGGG TTGGCCACTG  
 15 6 P S V F P L A P S S K S T S G G T A L V K D Y F P E P V T

**FIG.-31**

1401 GGTTCTGGG AACTCAGGGG CCCTGACCAAC CGGGTGGCAC ACCTTCCCCG CTGCTCAGCA GTCCCTTACA CTCTACTCCC TCAGGAGGT GGTGACCGT  
CCACAGCACC TTGAGTCCCCG GGGACTGGTC GCGGACTGGC GCGGACTGGT TGGAGGGGG GACAGATGT CAGGAGTCT GAGATGAGGG AGTCGTCGCA CCACTGGCAC  
159 V S W N S G A L T S G V H T F P A V L Q S G L Y S L S S V V T V

1501 CCCTCAGCA GCTTGGCAC CCAGACTAC ATCTGCAACG TGAATCACAA GCCCAGCAAC ACCAACGGTCG ACAAGAAAGT TGAGGCCAA TCTTGTGACA  
GGGAGGTGTT CGAACCGAC CGCTGGATG TAGACGTTGC ACTTAGTGT CGGCTCGTTG TGGTTCAGGC TGTCTTCA ACTCGGGTT AGAACACTGT  
192 P S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K

1601 AAACTAACGG CGGCATGAAA CAGCTAGAGG ACAAGGTGAA AGAGCTACTC TCCAGAAACT ACCACCTAGA GAATGAAGTG GCAAGACTCA AAAAACCTGT  
TTTGAGTGCC GGGGTACTTT GTCGATCTCC TGTCTGAG AGGTCTGTGA TGGTGGATCT CTTACTTCAC CGTTCTGAGT TTTTGAAACA

226 T H G R M K Q L E D K V E E L L S K N Y H L E N E V A R L K K I V

^end of heavy chain, start of leucine zipper

1701 CGGGAGGCC GCAAAGCTTA GTGGGGGTGG CTCGGGTCC GGTGATTG ATTATGAAA GATGGCAAC GCTATAAGG GGGCTATGAC CGAAATGCC  
GCCCTCGCG CCGTCGAAT CACCGCACC GAGACCAAGG CCACTAAAC TAATACTTTT CTACCGTTG CGATTATTC CCCGATACTG GCTTTTACGG  
259 G E R G K L S G G S G D F D Y E K M A N A N K G A M T E N A

^end of leucine zipper

^ gene III coat protein (267-end)

1801 GATGAAACG CGCTACAGTC TGACGCTAA GGCACAACTTG ATTCTGCTGC TACTGATTAC GGTCGCTGCTA TCGATGGTT CATGGTGCAC GTTTCCGGCC  
CTACTTTGCG GCGATGTCAG ACTGGGATTTCGACTGGGATTAAC TAAGACAGCG ATGACTAATG CCACGACGAT AGCTACCAA GTCACACTG CAAAGGCCGG  
292 D E N A L Q S D A K G K L D S V A T D Y G A A I D G F I G D V S G L

1901 TTGCTAATGG TAATGGTGT ACTGGTGAATT TTGCTGGCTC TAATTCACCA ATGGCTCAAG TGGGTGACGG TGATTAATGA CCTTTAATGA ATAAATTCCG  
AACGATTACCA ATTACACGA TGACCACTAA AACGACCGAG ATTAAAGGGTT TACCGACTTC AGCCACTGGC ACTATAAGT GGAATTACT TATTAAGGC  
326 A N G N G A T G D F A G S N S Q M A Q V G D G D N S P L M N N F R

2001 TCAATATTTA CCTTCCCTCC CTCAATGGT TGAATGTCGC CCTTTTGTCT TTAGGGCTGG TAAACCATAT GAATTTCATA TTGATTTGCA CAAATAAAC  
AGTTATAAT GGAAGGGAGG GAGTTAGCC ACTTACAGCG GGAAACAGA ATTCGGGACCG 359 Q Y L P S L P Q S V E C R P F V F S A G K P Y E F S I D C D K I N

46/75

2101 TTATTCGGT GTGCTTGC GTTCTTTTA TATGGTGCCTA CCTTTATGTA TGTATTTCT ACGTGTTGCTA ACATACTGCG TAATAAGGG TCTTAA  
AATAAGGCAC CACAGAAACG CAAAGAAAT ATACAAACGGT GGAAATACAT ACATAAAAGA TGCAAACGAT TGTATGACGC ATTATTCCTC AGAATT  
392 L F R G V F A F L L Y V A T F M Y V F S T F A N I L R N K E S O

**FIG. 31.C**

1 GAATTCAACT TCTCCATACT TGGATAAGG AAATAACAGAC ATGAAAATC TCATTGGCTGA GTTGTATTTC AAGCTTGCCC AAAAGAGA AGAGTCGAAT  
CTTAAGTGA AGAGGTATGA AACCTATTCC TTATGTCG TACTTTAG AGTAACGACT CAACAATAAA TTGAAACGGG TTTTCTCT TCTCAGCTTA

101 GAACTGTGT CGCAGGTTAGA AGCTTGGAG ATTATGCTCA CTGCAATGCT TCGCAATATG GCGAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG  
CTTGACACAC GGGCCATCT TCGAAACCTC TAATGGCTG GACGTTACGA AGCGTTACGA AGCGTTAC CGCGTTTAC TGCTTGTGCG CAACTAACTA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAG CCCGATGCCA GCATTGCTGA CGACCGATACG GACCTGCTGC GCGATTACGT AAACAGTAA TTGAAGCATC CTCGTCAGTA  
CCCCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTCTTCAAT AACCTCGTAG GACGACTCAT

301 AAAAGTTAAT CTTTCAACA GCTGTATAA AGTTGTCACG GCGGAGACTT ATAGTCGCTT TGTTTTATT TTTTAATGTA TTGTAACTA GTACGCAAGT  
TTTCAATTA GAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGGAA ACAAAATAA AAAATTACAT AACATTGAT CATGGTTCA

401 TCACGGAAAA AGGGTATGTA GAGGTGAGG TGATTTATG AAAAGATA TCGATTCTC TCGATTCTC ATGTCGCTT TTTCATATGC TACAAATGCC  
AGTGCAATTTC TCCATACAT CTCCAATCC ACTAAAATAC TTTCATTTAGCTT AGCCTAAAGA AGAACGTAGA TACAGCAA AAAGATAACG ATGTTACGG  
0

M K N I A F L L A S M F V F S I A T N A  
^start of still signal sequence

47/75

501 TATGGAGATA TCAAGATGAC CCAGTCCCCG AGCTCCCTGT GGGGATAGG GTCAACATCA CCTGGCGTGC CAGTCAGGAT GTGTCACTG  
ATACGTCTAT AGGTCTACTG GGTCAAGGGGC TCGAGGGACA CCCGCTATCC CAGTGGTAGT GGACGGCAGC GTCAAGTCTTA CACAGGTGAC  
21 Y A D I Q M T Q S P S L S A S V G D R V T I T C R A S Q D V S T A  
^start of light chain

^EcorV

601 CTGTAGCCCTG GTATCAACAG AAACCGGAA AAGCTCCGAA GCTTCTGATT TACTCGGAT CCTTCCTCTA CCTCTGGAGTC CCTTCCTGGCT TCTCTGGTAG  
GACATCGGAC CATACTGTCTC TTTCGCTCTT TTTCGAGGCTT CGAAGACTAA ATGAGCCGTA GGAAAGGAGAT GAGACCTCAG GAAGAGCGA AGAGACCATC  
55 V A W Y Q Q K P G K A P K L I Y S A S F L Y S G V P S R F S G S  
^start of light chain

601 CTGTAGCCCTG GTATCAACAG AAACCGGAA AAGCTCCGAA GCTTCTGATT TACTCGGAT CCTTCCTCTA CCTCTGGAGTC CCTTCCTGGCT TCTCTGGTAG  
GACATCGGAC CATACTGTCTC TTTCGCTCTT TTTCGAGGCTT CGAAGACTAA ATGAGCCGTA GGAAAGGAGAT GAGACCTCAG GAAGAGCGA AGAGACCATC  
55 V A W Y Q Q K P G K A P K L I Y S A S F L Y S G V P S R F S G S  
^start of light chain

701 CGGTTCCGG ACGGATTTCAT CTCGACCAT CAGCAGTCTG CAGCCGGAA ACTTCGCAAC TTATTACTGT CAGCAATCTT ATACTACTCC TCCCACGTT  
GCCAAGGCC TGGCTAAAGT GAGACTGGTA GTGTCAGAC GTCGGGCTTC TGAAGCGTGT AATAATGACA GTCCGTAGAA TATGATGAGG AGGGTGCAG  
88 G S G T D F T L T I S S L Q P E D F A T Y Y C Q Q S Y T T P P T F  
^CDR-L3

FIG.-32A

1 GGACAGGGTA CCAAGGTTGA GATCAAACGGA ACTGTGGCTG CACCATCTGT CCTCATCTCTG ATGAGGAGTT GAAATCTGGA ACTGCCTCTG  
 CCTGTCCCAT GGTTCCACT CTAGTTGCT TGACACCGAC GTGGTAGACA GAAGTAGAAAG GGCGGTAGAC TACTCGTCAA CTTIAGACCT TGACGGAGAC  
 1 G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V  
 ^KpnI

1 TTGTGTGCCT GCTGAATAAC TTCTATCCCA GAGAGGCCAA AGTACAGTGG AAGGTGGATA ACGCCCTCCA ATCGGGTAAAC TCCCAGGAGA GTGTCACAGA  
 AACACACGGA CGACTATTG AGATAGGGT CTCTCGGTT TCATGTCAAC TTCCACCTAT TGCGGGAGGT TAGCCCCATTG AGGGTCCTCT CACAGTGTCT  
 5 V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E

1 GAGGACAGC AAGGACAGCA CCTACAGGCC CAGCAGGACC CTGACCGCTGA GCAGAACGGAGA CAAAGAGCTT ACGGCTGTGGAA AGTCACCCAT  
 CCTCCCTGTG TTCCCTGTCTG TTCCCTGTCTG GGTATCGGA GTCGTGTGG GACTGCGACT CGTTTCGTCT GATGCTCTTT GTGTTTCAGA TGCGGACGCT TCACTGGGTA  
 8 Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H  
 ^end of light chain, start of gd tag

48/75

1 CAGGGCCTGA GCTGCCCGT CACAAAGAGC TTCAACAGGG GAGAGTGTGG TGCCAGCTCC GGTATGGCTG ATCCGAACCG TTTTCGCGGT AAGGACCTGG  
 GTCCCGGACT CGAGGGGCA GTGTTTCCTCG AAGTTGTCCC CTCTCACACC ACGGTCGAGG CCATACCGAC TAGGCTTGGC AAAGGGCCA TTCCTGGACC  
 10 Q G L S S P V T K S F N R G E C G A S S G M A D P N R F R G K D L A  
 ^end of light chain, start of gd tag

1 CATAACTCGA GGCTGATCCCT CTACGCCGGGA CGGCATCGTGG CCCTAGTACG CAAGTTACG TAAAGGGT AACTAGAGGT TGAGGGTATT TTATGAAAAA  
 GTATTGAGCT CCGACTAGGA GATGCGGCCT GCGTAGGCC ACCGATCATGC GTTCAAGTGC ATTTCCTCCA TTGATCTCA ACTCCACTAA AATACTTTT  
 15 0  
 3  
 M K K  
 ^start of stII  
 ^start of heavy chain  
 ^BsiWI

**FIG. 32-8**

1401 CCAGGGGGCT CACTCCGTT GTCTGTGCA GCTCTGGCT TCACCTTAG TAGGTTCTGG ATACACTGGG TGGGTCTAGGC CCCGGGTAAG GGCCTGGAA  
GGTCCCCGA GTGAGGCAA CAGGACACGT CGAAGACCGA AGCTGGAATC ACCAAGAACC TATGTGAAAC CCGAGTTCG GGGCCCATTC CGGGACCTTA  
14 P G S L R I S G F T I S G S W I H W V R Q A P G K G L E W  
^CDR-H1

1501 GGTTGGCTTG GATTGGCTCC TATAGGGCG CTACTGACTA TGCCGATAGC GTCAAGGGCC GTTTCACAT AAGGCAGAC ACATCCAAA ACACAGCCTA  
CCCAACGAAC CTAACGAGGA ATATGCCGC GATGACTGAT ACCGGCTATCG CAGGTCGGG CAAAGTGATA TTCGCGTCTG TGTAGGGTT TGTGTCGGAT  
48 V A W I A P Y S G A T D Y A D S V K G R F T I S A D T S K N T A Y  
^CDR-H2

1601 CCTACAAATG AACAGCTTA GAGCTGAGGA CACTGCCGTC TATTATTGTG CAAGAGAGG GGGCTTGATAC TGGGTGTTGC ACTACTGGG TCAAGGAACA  
GGATGTTAAC TTGTCGAATT CTCGACTCCT GTGACGGCAG ATAATACAC GTTCTCTCCC CCCGAAATG ACCACAAGC TGTAGACCCC AGTTCTGT  
81 L Q M N S L R A E D T A V Y Y C A R E G L Y W V F D Y W G Q G T  
^CDR-H3

1701 CTAGTCACCG TCTCCTGGC CTCCACCAAG GCCCCATCGG TCTTCCCTT GGCACCCCTCC TCCAAGAGCA CCTCTGGGG CACAGGGCC CTGGGCTGCC  
GATCAGTGGC AGAGGAGCCG GAGGTGGTTC CCGGGTAGCC AGAAGGGGA. CCGGGGAGG AGGTCTCGT GGAGACCCC GTGTCGCCG GACCCGACGG  
114 L V T V S S A S T K G P S V F P L A P S S K S T S G G T A A L G C L  
^ApaI

1801 TGGTCAAGGA CTACTCCCC GAACCGGTGA CGGTGCTGG GAACTCAGGC GCCCCGACCA CACCTTCCCG GCTGTCCTAC AGTCCTCAGG  
ACCACTTCCT GATGAAGGGG CTTGGCACT GCAACAGGCAC CTTGAGTCCG CGGGACTGTT CGGGCACGT GTGGGAGGGC GCAGAGATG TCAGGAGTCC  
148 V K D Y F P V T V S W N S G A L T S G V H T F P A V L Q S S G  
^49/75

1901 ACTCTACTCC CTCAGCAGCG TGGTGAACCGT GCCCTCCAGC AGCTTGGCA CCCAGACCTA CATCTGCAAC GTGAATCACA AGCCAGCA CACCAAGGTC  
TGAGATGAGG GAGTCGTGCG ACCACTGGCA CGGGAGGTGG TCGAACCCGT GGGCTGGAT GTAGACGTG CACTAGTGT TGGGTCTGT GTGGTCCAG  
181 L Y S L S S V V T V P S S S I G T Q T Y I C N V N H K P S N T K V

2001 GACAAGAAAG TTGAGCCAA ATCTTGTGAC AAAACTCACC TCTAGAGTGG CGCTGGCTCT GTGCTGGTT ATGCTGGTT GCCGGGGC GTTTTTATG  
CTGTTCTTC AACTCGGGTT TAGAACACTG TTGTGAGTGG AGATCTCACCC GCAACCGAGA CCAAGGCAAC TACGAGCCAA CGGGGGCG CAAAAAATAC  
214 D K V E P K S C D K T H L O

2101 CTAGGCCGC CCTATACCTT GTCTGCCTCC CGCGTGTGCA TGGAGCCGG CCACCTCGAC CTGAAATGAA GCCGGGGCA CCTCGCTAAC  
GATCGGGCG GGATATGAA CAGACGGAGG GCGGCAACGC AGCGCCACGT ACCTCGGGCC CGTGGAGCTG GACTTACCTT CGGGCCCGT GGAGCGATTG

**FIG. - 32 C**

2201 GGATTCACCA CTCCAAGAAAT TGGAGCCAAT CAAATTCTTGC GGAGAACTGT GAATGCGCAA ACCAACCCATT GGCAGAACAT ATCCATCGCG TCCGCCATCT CCTAAGTGGT GAGGTCTTAA ACCTCGGTAA GTTAAGAACG CCTCTTGTAA CTTACGACA CTTACGGTGT TGGTGGAA CCGTCTTGTAA TAGGTGGCGC AGGGGGTAGA

2301 CCAGCAGCCG CACGGGGCG ATCTCGGGCA GCGGTGGTC CTGGCACCG GTGGCATGA TCGTGGTCTCT GTCGTTGAGG ACCCGGTAG GCTGGGGGG GGTGCGGC GTGGCGGC TAGAGCCGT CGAACCCAG GACCGTGC CACGGTACT AGCACGAGGA CAGCAACTCC TGGCCGATC CGACCCCCC

2401 TTGCTTACT CGTAGCAGA ATGAATCACC GATAACGGAG CGAACGTGAA CGGACTGTGT CTGCAAAACG TCTGCCACCT GAGCAACAC ATGAATGGTC AACGGAATGA CCAATCGTCT TACTAGTGG CTATGGCTC GCTTGCACCT CGCTGACGAC GACGTTTGC AGACGCTGGA CTCGTTG TACTTACAG

2501 TTTCGGTTTC CGTGTTCGTA AAGTCGGAA ACGGGAACT CAGGCCCTG CACCATTTAG TTCCGGATCT GCATCGCAGG ATGCTGCTGG CTACCTGTG AAGCCAAGG CACAAAGCAT TTCAAGACCTT TGGCCTTCA GTCGGGAC GTGTTATAC AAGGCCTAGA CGTAGCGTCC TAGACGACCG ATGGGACAC

2601 GAAACACCTAC ATCTGTATTA ACGAAGGGCT GGCATTGACC CTGAGTGATT TTCTCTGGT CCCGCCAT CCATAACGCC AGTTGTTAC CCTCACAAACG CTTGGGATG TAGACATAAT TGCTTCGGA CGTGTAACTGG GACTCACTAA AAAGAGACCA GGGGGCGTA GGTATGGGG TCAACAAATG GGAGTGTG

2701 TTCCAGTAAC CGGGCATGTT CATCATCAGT ACCCGTATC GTGAGCATCC TCTCTGGT CATCGGTATC ATTACCCCA TGAACAGAAA TTCCCCCTTA AAGGCTATTG GCCCTTACAA GTAGTACTCA TTGGGATAG CACTCTAG AGAGACAA GTAGCCATAG TAATGGGGT ACTTGTCTT AAGGGGAAT

2801 CACGGAGCA TCAAGTGAAC AACACGCCCT TAACATGGCC CGCTTATCA GAGGCCAGAC ATTAAACGCTT CTGGAGAAAC TCAACGAGCT GTGCTCCGT AGTTCACTGG TTGTCCTT ATTGTACCG GCGAAATAGT CTTGGCTCTG TAATTGCGAA GACCTCTTGG AGTGTCTCGA

2901 GGACGGGAT GAACAGGAG ACATCTGTGA ATCGCTTCAC GACCACGGCTG ATGAGCTTA CGCGAGGATC CGGAATTGT AACACGTTAT ATTGTGTTAA CCTGGCCTA CTTGTCCTG TGAGGACACT TAGCGAAAGTG CTGGTGGCAG TACTGAAAT GGCTCTCTAG GCCTTAACA TTGGCAATTAAACATT

3001 AATTGGGTT AAATTGTTGT TAAATCAGT CATTTTTAA CCAATGGCC GAAATGGCA AAATCCCTTA TAAATCAAAA GAATAGACCG AGATGGGTT TTAAGGGCAA TTAAAAACA ATTAGTCGA GTAAAAAAT GGTTATCCGG CTTAGGCCGT TTAGGAAAT ATTAGTTT CTATCTGGC TCTATECCAA

3101 GAGTGGTT CGAGTTGGA ACAAGAGTCC ACTATTAAG AACGTGACT CCAACGTCAA AGGGGAAA ACCGTCTATC AGGGCTATGG CCCACTAGT CTCACAAACAA GCTCAAACCT TGTTCAGG TGATTAATTG TTGCACTGAA GGTTGCAGTT TCCCGCTTT TGGCAGATAG TCCCGATACC GGGTGTGCA

3201 GAACCATCAC CTTAATCAAG TTTTTTGGGG TCGAGGTGCC GTAAACCACT AAATCGGAAC CCTAAACGGGA CCCCCGATT TAGAGCTGA CGGGAAAGC  
 CTTGGTAGTG GAATTAGTTC AAAAACCCC AGCTCCACGG CATTTCGTA TTATTCGTA TTAGGCTTG GGATTTCCCT CGGGGCTAA ATCTCGAATC GCCCTTTCG  
  
 3301 CGCGAACGT GCGGAGAAAG GAAGGGAAAGA AGGGAAAGG AGGGGGCGCT AGGGGGCTGG CAAGTGTAGC GGTACGCTG CGGTAAACCA CCACACCGC  
 GCCGCTTGCA CGCGCTTTC CTTCCCTCTC TTGCTTTC CTCGCGCTT TCGGGCGGA TCCGGCGGA GTTACATCG CCAGTGGAC GCGCATGGT GGTGCCCC  
  
 3401 CGCGCTTAAT GCGCCGCTAC AGGGGGCGTC CGGATCCTGC CTCGGCGGT TCGGTGATGA CGGTGAAAC CTCGACACA TCGAGCTCCC GGAGACGGC  
 CGCGGAATTA CGCGGGATG TCCCGGCGAG GCTAGGACG GAGGGCCAA ACCCACTACT GCCACTTTC GAGAACGTGT ACGTGAGGG CCTCTGCCAG  
  
 3501 ACAGCTTGTTC TGTAAAGGGGA TGCGGGGAGC AGACAAGCCC GTCAAGGGGC GTCAAGGGGT GTGGGGGT GTCGGGGGC AGCCATGACC CAGTCACGTA  
 TGTGAAACAG ACATTCGCTT ACGGCCCTCG TCTGTTGGG CAGTCCGGG CAGTCGCCA CAACGCCA CAGGCCGG TCGGTACTGG GTCAAGTGCAT  
  
 3601 GCGATAGCGG AGGTATACT GGCTTAACTA TGCGGCATCA GAGCAGATG TACTGAGAGT GCACCATATG CGGTGTGAA TACCGCACAG ATGCCAAAGG  
 CGCTATCGCC TCAATATGA CCGAATTTGAT ACGCCGTAGT CTGCTCTAAC ATGACTCTCA CGTGGTTATAC GCCACACTT ATGCCGTGTC TAGGCAATTCC  
  
 3701 AGAAATACC GCATCAGGG CTCTTCGCT TCCCTCGCTCA CTGACTCGCT GCGCTCGTC GTTCGGCTGC GGCAGGGGT ATCAGCTCAC TCAAGGGGG  
 TCTTTTATGG CGTAGTCCCG GAGAAGGGGA AGGAGCCAGT GACTGAGCGA CGCGAGCCAG CAAGCCGAGC CCGCTCGCCA TAGTCGAGTG AGTTTCGCC  
  
 3801 TAATACGGTT ATCCACAGAA TCAGGGGATA ACCCAGAAA GAACATCTGA GCAGAAAGGC AGCAAAAGGC CAGGAACCGT AAAAGGCC CGTTGCTGGC  
 ATTATGCCAA TAGGTGTCTT AGTCCCTAT TGGGCTCTT CTTGTAACACT CGTTTCCGG TCGTGTTCCGG GTCCCTGGCA TTTTTCGGC GAAACGCC  
  
 3901 GTTTTCCAT AGGCTCCGCC CCCCTGACGA GCATCACAAA AATCGACGCT CAACTCAGAG GTGGGAAAC CCGACAGGAC TATAAAGATA CCAGCGTT  
 CAAAAAGGTAA TCCGAGGGGG GGGGACTGCT CGTACTGTT TTAGGTGCGA GTTCAGTCTC CACCGCTTTCG ATATTCTAT GGTCCGAAA  
  
 4001 CCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTCCGGACCC TGGCGCTTAC CGGATACTCG TCCGCTTTC TCCGCTTCCG AAGCGTGGCG CTTTCTCATA  
 GGGGGACCTT CGAGGGAGCA CGGAGAGGA CAAAGGCTGG ACGGCGAATG GCCTATGGAC AGGGGAAAG AGGGAGCCC TTGCGACCGC GAAAGAGTAT  
  
 4101 GCTCACGCTG TAGGTATCTC AGTTGGTGT AGGTGTTGC CTCCCAAGCTG GGCTGTTGC ACAGAACCCC CGTTAGCCC GACCGCTGGC CCTTATCCGG  
 CGAGTGGAC ATCCATAGAG TCAAGCCACA TCCAGGAAG CAGGTTCGAC CCGACACAGC TGGTTGGGG GCAAGTCGGG CTGGCGACGC GGAATAGGCC  
  
 4201 TAACTATCGT CTTGAGTCCA ACCCGGTAAAG ACACGACTTA TCGGCCACTGG CAGCAGCCAC TGGTAACAGG ATTACGAGG CGAGGTATGT AGGGGGTGT  
 ATTGATAGCA GAACTCAGGT TGGCCATTIC TGTGCTGAAT AGGGGTGACCGT GTCGTGGTG ACCATTGTCTC GCTCCATACA TCCGCCACGA

4301 ACAGAGTTCT TCAAGTGGTG GCCTAACTAC GGCTACACTA GAAGGACAGT ATTGGTATC TGGGCTCTGC TGAAGCCAGT TACCTTGGGA AAAAGAGTTG  
TGTCTCAAGA ACTTCACAC CGGATTGATG CCGATGTAT CTTCCTGTCA TAAACCATTAG ACGCGAGACG ACTTCGGTCA ATGGAAGCCT TTTCCTCAAC

4401 GTAGCTCTTG ATCCGGCAA CAAACCACCG CTGGTAGGG TGCGTTTTT GTTGCAGGAC AGCAGATTAC GCGCAGAAA AAAGGATCTC AAGAAGATCC  
CATCGAGAAC TAGGGCGTT GTTGGTGGC GACCATCGCC ACCAAAAAA CAAACGTTG CGTCTAATG CGCGCTTTT TTTCCTAGAG TTCTTCTAGG

4501 TTGTATCCTT TCTACGGGGT CTGACGCTCA GTGGAACGAA AACTCACGTT AAGGGATTG GTTCATGAGA TTATCAAAA GGATCTTCAC CTAGATCCTT  
AAACTAGAAA AGATGCCCA GACTGGAGT CACCTTGCTT TTGAGTGGAA TTCCCTAAA CCAGTACTCT AATAGTTT CCTAGAAGTG GATCTAGGAA

4601 TTAATTAAA ATGAAAGTT TAAATCAATC TAAAGTATAT ATGAGTAAAC TTGGTCTGAC AGTTACCAAT GCTTAATCAG TGAGGGCACCT ATCTAGCGA  
AATTAAATT TTACTTCAAA ATTAGTTAG ATTCAATATA TACTATTG AACCAAGACTG TCAATGGTTA CGAATTAGTC ACTCCGTGGA TAGAGTCGCT

4701 TCTGCTTATT TCGTTCATC ATAGTGTGCT GACTCCCCGT CGTGTAGATA ACTTACGATAAC GGAGGGCTT ACCATCTGGC CCCAGTGTG CAATGATAAC  
AGACAGATAA AGCAAGTAGG TATCAACGGA CTGAGGGGA TGGTAGACCG CCCTCCCGAA TGGTAGCTATG GGTCACGAC GTTACTATGG

4801 GCGGAGACCA CGCTCACCGG CTCCAGATTT ATCAGCAATA AACCAAGCCAG CGGGAAAGGGC CGAGCGAGA AGTGGTCCCTG CAACTTTATC CGCCCTCCATC  
CGCTCTGGGT CGGAGTGGCC GAGGTCTAAA TAGTGTATT TTGGTCTGGTC GGCTTTCGGCG GCTCGCTCT TCACCAAGGAC GTTGAATAG GCGGAGGTAG

4901 CAGCTTATA ATGGTGTGGG GGAAAGCTTAA GTAAAGTGTGTT CGCCAGTTAA TAGTTTGCGC AACGTTGGTGC CCATGCTGC AGGCATCTGT GTGTCACGCT  
GTCAAGATAAT TAAACAACGCC CCTTCCGATCT CATTCACTAA GCGGTCAATT ATCAAACGCC GGTAACGACG TCCGTAGCAC CACAGTGGGA

5001 CGTGGTTGG TATGGCTCA TTCAAGTCCCG GTTCCCAACG ATCAAGGGGA GTTACATGAT CCCCATGTT GTGAAAGAAA GCGGTTAGCT CCTTTCGGTCC  
GCAGGAAACC ATACCGAAGT AAGTCAGGC CAAGGGTTGC TAGTTCGGCT CAATGTACTA GGGGGTACAA CACGTTTTT CGCCAATCGA GGAAGGCCAGG

5101 TCCGAGTGGT GTCAAGAAGTA AGTGGTATCA CTCATGGTTA TGGCAGGACT GCATTAATTCT CTTACTGTCA TGCCATCCGT AAGATGCTT  
AGGCTAGCAA CAGTCTCAT TCAACGGGG TCACAAATAGT GAGTACCAAT ACCGTCGTGA CGTATTAGA GAATGACAGT ACGGTAGGA TTCTACGAAA

5201 TCTGTGACTG GTGAGTACTC AACCAAGTCA TTCTGAGAAT AGTGTAGG GCGACCGAGT TGCTCTGCC CGGGCTCAAC ACGGGATAAT ACCGGCCAC  
AGACACTGAC CACTCATGAG TTGGTTAGT AAGACTCTTA TCACATACGC CGCTGGCTCA ACGGAAACGG GCCGCAAGTG TGGCCTATTA TGGCGGGTG

5301 ATAGGAGAAC TTAAAAGTG CTCATCATTTG GAAAACGTTTC TICGGGGCGA AACTCTCAA GGATCTTACCG GCTGTTGAGA TCCAGTTCGA TGTAAACCCAC  
TATCGTCTTG AAATTTTCAC GAGTAGTAAC CTTTTCGAAG AAGCCCCGCTT TTGAGAGTT CCTAGAATGG CGACAACCT AGGTCAAGCT ACATGGGTG  
5401 TCGTGCACCC AACTGATCTT CAGCATCTT TACTTTCAAC AGCGTTTCTG GGTGAGCAAA AACAGGAAGG CAAATGCCG CAAAAGGG AATAAGGG  
AGCACCGTGGG TTGACTGAA GTCGTAGAA ATGAAAGTGG TCGAAGAC CCACTCGTTT TTGTCCTCC GTTTACGGC GTTTTTCCTC TTATCCGC  
5501 ACACGGAAAT GTTGAATACT CATACTCTTC CTTTTCAAT ATTATGAG CATTATCAG GGTTATTGTC TCATGAGCGG ATACATATT GAATGTTATT  
TGTGCCTTA CAACTTATGA GTATGAGAAG GAAAAGTTA TAATACTTC GTAAATACAG AGTACTCGCC TATGTAAAAA CTTACATAAA  
5601 AGAAAATAA ACAAAATAGGG GTTCCGGCGA CATTTCGGCG AAAAGTCCAAC CCTGACGCTT AGAAACCAT TATTATCATG ACATAACCT ATAAAATAG  
TCTTTTATT TTGTTATCCC CAAGGGCGT GTAAAGGGT TTTCACGGT GGACTGCGA TTCTTGGTA ATAATAGTAC TGTAAATTGGA TATTTTTAC  
5701 GCGTATCAGC AGGCCCTTTC GTCTTCAATA CAGGTAGAC TTTCTGAGAG ATGTAACAGTG AAATCCCGA AATATACAC ATGACTGAAG GAAGGGAGCT  
CGCATAGTGC TCCGGAAAG CAGAAAGTTAT GTCCATCTGG AAAGCATCTC TACATGTCAC TTIAATATGTG TACTGACTTC CTTCCCTCGA  
5801 CGTCATTCCC TGCCTGGTTA CGTCACCTAA CATCACTGTT ACTTTAAAAA AGTTTCCACT TGACACTTG ATCCCTGATG GAAAACGAT AATCTGGAC  
GCAGTAAGGG AGGGCCCAAT GCAGTGGATT GTAGTGACAA TGAAATTTTT TCAAGGTGA ACTGTGAAAC TAGGGACTAC CTTTGGGTA TTAGACCTG  
5901 AGTAGGAAAGG CTTTCATCAT ATCAAATGCA AGTACAAAG AAATAGGGCT TCTGACCTGT GAAGCAACAG TCAATGGCA TTGTTATAAG ACAAACTATC  
TCATCTTTC CGAAGTAGTAA TAGTTACGT TGCTATCCGA AGACTGGACA CTTCGTTGTC AGTACCCGT AAACATATC TGTGTTGATAG  
6001 TCACACATG ACAAAACCAAT ACAATACAGG TAGACCTTTC GTAGAGATGT ACAGTGAAT CCCGAAATT ATACACATGA CTGAAGGAAG GGAGCTCGTC  
AGTGTAGC TTGTTGGTTA TGTATGTC ATCTGGAAAG CATCTCTACA TGTCACTTTA GGGCTTTAA TAGTGTACT GACTTCCTTC CCTCGAGCAG  
6101 ATTCCTGTC GGGTACGTC ACCTAACATC ACTGTTACTT TCCATGTTGAC ACTTTGATCC CTGATGGAA ACCGATAATC TGGGACAGTA  
TAAGGACGG COCAATGCG TGGATTGAG TGACAATGAA ATTTTCAA AGGTGAACCTG TGAACACTGG GACTACCTT TGGCTATTAG ACCCTGTCT  
6201 GAAAGGGCTT CATCATATCA AATGCAACGT ACAAAAGAAAT AGGGCTCTG ACCTGTGAAG CAACAGTCAA TGGCATTG TATAAGACAA ACTATCTCAC  
CTTTCGGCAA GTAGTATAGT TTACGTGCA TTGTTCTTTA TCCCGAAGAC TGGACACTTC GTGTCACTT ACCGTAAC ATATTCTGTT TGATGAGTG  
6301 ACATGGACAA ACAAAACAA TCTACAGGTA GACCTTTCGT AGAGATGTAC AGTGAATTC CGAAATTAT ACATGACT GAGGAAGGG AGCTGTCAT  
TGTAGCTGTT TGTTATGTT AGATGTCAT CTGGAAAGCA TCTCTACATG TCACTTAGG GGCTTTAATA TGTGTAATC CTTCCTTCCC TCGAGCTA  
6401 TCCCTGCCGG GTACGTCAC CAAACATCAC TGTACTTTA AAAAAGTTTC CACTTGACAC TTGATCCCT GATGAAAC GATAATCTG GGACAGTAA  
AGGGACGGCC CAATGCGAGTG GATTGTAAGC ACAATGAAAT TTGTCAAAG GTGAACCTG AAACAGGAA CTACCTTTG GTTAACTGAC CCTGTCATCT  
6501 AAGGGCTCA TCATATCAA TGCAACGCA AGGAAATAG GGCTCTGAC CTGTGAAGCA ACAGTCATG GGCATTGTA TAAGACAAAC TATCTCAC  
TTCCGGAAAGT AGTATAGTT ACCTGTCATG TTTCCTTATC CGAAGACTG GACTCTCGT TGTCACTAC CCGTAAACAT ATTCTGTTG ATAGAGTGTG  
6601 ATCGACAAAC CAAATACAATC  
TAGCTGTTTG GTATGTTAG

FIG.\_32\_G

1 TTCGAGCTCG CCCGACATTG ATTATTGACT AGTATTAAAT AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCGGC GTTACATAAC  
AAGCTCGAGC GGGCTGTAAC TAATAACTGA TCAATAATTAA TCATTAGTTA ATGCCCACTT AATCAAGTAT CGGGTATATA CCTCAAGGG CAATGTTATG  
101 TTACGGTAAA TGGCCGGCTT GGCTGACGCC CCAACGACCC CGGCCCATTT ACGTCATAAA TGACGTATGT TCCCATAGTA AGGCCAATAG GGACTTCCA  
AATGCCATT ACCGGGGAA CGGACTGGCG GGTGCTGGG GGGGGTAAAC TGGAGTTATT ACTGCAATTACAGGGTATCAT TGGGTATTC CCTGAAAGGT  
201 TTGACGTCAA TGGGGAGT ATTACGTA AACTGCCAC TTGGCAACTAC ATCAAGTGTAA TCAATAGCCA AGTAGCCCC CTAATGACGT CAATGACGGT  
AACTGCAAGTT ACCACCTCA TAAATGCACT TTGACGGGT AACCGTCAATG TAGTCACAT AGTAACTGGT TCATGGGGG GATAACTGCA GTTACTGCCA  
301 AAATGGCCCG CCTGGCATA TGGCCAGTAC ATGACCTTAT GGACTTTC TACTGGCAG TACATCTACG TATTAGTCAT CGCTATTACCG ATGGTGATGC  
TTTACGGGC GGACCGTAAT ACGGGTCAAT TACTGGAATA CCCTGAAAGG ATGAAACCGTC ATGTAATGCA ATAATAGTA GGATAATGG TACCAACTACG  
401 GGTGGCA GTACATCAAT GGGCGTGGAT AGCGGTGAT TTTCAGTCAGTAC CTCACGGGA TTTCAGTCAGTAC TCCACCCCAT TGACGTCAAT GGAGTGTGT TTTGGCACCA  
CCAAAACCGT CATGTAGTT CCCGCACTTA TCGCCTAACT GAGTGCCTCT AAAGGGTCAG AGGTGGGTAA ACTGCAAGTTA ACTGCAAGTTA CCTCAAAACA AAACCGTGGT  
501 AAATCAACGG GACTTTCCAA AATGTCGTA CAACCTCCGCC CCATTGACGC AAATGGGGG TAGGGCTGTA CGGTGGGAGG TCTATATAAG CAGAGCTGGT  
TTAGTGCCT CTGAAAGGTT TTACAGCATT GTTACAGCATT GTTACCGCC TTACCGCC ATCCGGCACAT GCCACCTCC AGATATATTC GTCTCGAGCA  
601 TTAGTGAACC GTCAAGATGCC CTGGAGACGC CATCACCGCT GTTTGACCT CCATAGAAGA CACCGGGAC GATCCAGCCT CGCGGGCGGG GAACGGTGGC  
AATCACTGG CAGCTTAGGG GACCTCTGG GTAGGTGGCA CAAAACTGGA GGTATCTCT GTGGCCCTGG CTAGTCGGA GGGGCCGGCC CTTGCCACGT  
701 TTGGAACGG GATTCGGCGT GCCAAGAGGTG ACGTAAGTAC CGCCTATAGA GTCTATAGGC CCACCCCTT GGCTTGTAA GAACGGGGCT ACAATTAAATA  
AACCTTGCGC CTAAGGGCA CGGTTCTCACT TGCATTCACT GGGGATATCT CAGATATCCG GTTGGGGAA CGGAAGCAAT CTTGGCCGA TGTTAAATTAT  
801 CATAACCTTA TGTATCATAC ACATACGATT TAGGTGACAC TATAGAATTAA CATCCACTTT GCCTTGTAA CCACAGGTGT CCACCTCCAG GTCCAACIGC  
GTATTGGAAAT ACATAGTATG TGTATGCTAA ATCCACTGTG ATATCTTATT GTAGGTGAAA CGGAAGAGA GGTGTCACA GGTGAGGGTC CAGGGTGGCG  
901 ACCTCGGTTC TATGATTGA ATTCCACCAT GGGATGGTCA TGTATCATCC TTTTCTAGT AGCAACTGCA ACTGGAGTAC ATTCAAGTAT CCAGATGACC  
TGGAGCCAG ATAGCTAACT TAAGGTGGTA CCCTACCGT ACATAGTAGG AAGAGATCA TCGTTGACGT TGACCTCATG TAAGTCTATA GGTCTACTGG  
1 M G W S C I I L F L V A T A T G V H S D I Q M T  
^met

Start VL  
^EcoRV

FIG. - 33 A

1001 CAGTCCCCGA GCTCCCTGTG GGGATAGGG TCACCATCAC CTGCCGTGCC AGTCAGGATG TGTCCACTGC TGTAGCCCTGG TATCAAACAGA  
 GTCAGGGCT CGAGGGACAG CGGGAGACAC CCGCTATCCC AGTGGTAGTG GACGGGACGG TCAGTCTAC ACAGGTGACG ACATGGACC ATAGTTGTCT  
 25 Q S P S S I S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K ^CDR-L1

11101 AACCAAGAAA AGCTCCGAAG CTTCTGGATTC ACTCTGGATTC CTTCTGGATTC CTTCTGGCTT CTCCTGGTAGC GGTTCCGGGA CGGATTTCAC  
 59 TTGGTCCCTT TCGAGGGCTC GAAGACTAAA TGAGCCGTAG GAAGGGAGATG AGACCTCGGG GAGGACCATCG CCAAGGCCCT GCCTAAAGTG  
 P G K A P K L L I Y S A S F L Y S G V P S R F S G S G S G T D F T  
 ^CDR-I2

11201 TCTGACCATT AGCACTTCTGC AGCCGGAAAGA CTTCGCAACT TATTACTGTC AGCAATCTTA TACTACTCCT CCACGTTG GACAGGGTAC CAAGGGAG  
 AGACTGGTAG TCGTCAGACG TCGGCCCTCT GAAAGCGTGTGA ATAATGACAG TCGTTGAAT ATGATGGAGA GGGTGC AAGC CTGTCCCCATG GTTCACCTC  
 92 L T I S S I Q P E D F A T Y C Q Q S Y T T P P T F G Q G T K V E ^KpnI  
 ^CDR-L3

1301 ATCAAACGAA CTGTGGCTGC ACCATCTGTC TTCATCTTC CGCCATCTGA TGAGGAGTTG AAATCTGAA CTGCTTCTGT TGTTGTGCCTG CTGAATAACT  
 55/75 125 I K R T V A P S V F I F P P S D E Q I K S G T A S V V C L I N N F  
 ^ start human kappa

401	TCTATCCCAG AGAGGCCAAA	GtACAGTGGAA AGGTGGATAA	CGCCCTCCAA	TCGGGTAACt	CCCAGGAG	TGtCACAGAG	CAGGACACCA	AGGACAGCAC	
	AGATAGGGTC	TCTCCGGTTt	CATGTCACCT	TCCACCTATT	GGGGGGTT	AGCCCATTGA	GGGTCCCTC	ACAGTGTCTC	
159	Y P R E A K V Q W K V D N A L Q S G N S Q E S V T F Q D S K D S T								
501	CTACAGCCTC AGCAGGCC	TGACGGTGA	CAAGGAGAC	TACGAGAAC	ACAAAGTCTA	CGCCTGGAA	GTCACCCATC	AGGGCCTGAG	CTCGGCCGTC
	GATGTCGGAG	TGTCGTGGG	ACTGCGACTC	GTTCGTCTG	ATGCTCTTG	TGTTTCAGAT	GCGGACGCTT	CAGTGGTAG	TCCCCGGACTC
192	Y S L S S T L T L S K A D Y E K K V Y A C E V T H Q G L S S P V								

801 ACAAAAGCTT TCAACAGGGG AGAGTGTAAA GCTTGGCCGGC CATGGCCCAA CTTGTGTTATT GCAGGCTTATA ATGGTTACAA ATAAAGGCAAT AGCATCACAA  
8225 T K S F N R G E C O TGTGTTCTCGA AGTTGTCCCC TCTCACAAATT CGAACCGGGG GTACCGGGGT GAAACAATAA CGTCGAATAT TACCAATGTT TATTTCGTTA TCGTAGTGT

FIG. 33. B

1701 ATTTCACAAA TAAAGGCAATT TTTTCACTGC ATTCTAGTTC TGCTTTGTCC AAGCTCATCA ATGTATCTTA TCATGTCTGG ATCGGGAAATT ATTCGGGCC  
TAAAGTGTIT ATTTCGTAAG AAAAGTGACG TAGATCAAC ACCAAACAGG TTGAGTACTG TACATAGAAT AGTACAGACC TAGCCCTTAA TTAAGCCGGC

1801 AGCACCATGG CCTGAAATA CCTCTGAAAG AGGAACCTGG TTAGGATCT TCTGAGGGGG AAAGAACAG CTGAGGAAATG TGTTCTGGTC GACACCTTAC ACACAGTCAA TCCCACACCT  
TTCAGGGTCC CGAGGGGTG TCCGGTCTCA TAGGTTTCGT ACCTAGAGTT AATCACTGTT TGGTCCACAC CTTTCAGGGG TCCGAGGGT CGTCGCTT  
'change from C to T, kill KpnI site

1901 AAGTCCCAG GCTCCCGAG AGGCAGAAGT ATGCAAAGCA TGCATCTCAA TTAGTCAGCA ACCAGGTGTG GAAAGTCCCC AGGCTCCCCA GCAGGAGAA  
TTCAGGGTCC CGAGGGGTG TCCGGTCTCA TAGGTTTCGT ACCTAGAGTT AATCACTGTT TGGTCCACAC CTTTCAGGGG TCCGAGGGT CGTCGCTT

2001 GATGCAAAG CATGCCATCTC AATTAGTCAG CAAACCATAGT CCCGCCCTA ACTCCGCCCA TCCCGCCCT AACTCCGCCA AGTTCGGCC ATTCTCGCC  
CATACGTTTC GTACGTTAGAG TTAATCAGTC GTGGGTATCA GGGGGGGAT TGAGGGGGT AGGGGGGG A TTGAGGGGG TCAAGGGGG TAAGGGGG

2101 CCATGGCTGA CTAATTGTT TTATTATGC AGAGGGCGAG GCGGCCTCGG CCTCTGAGCT ATTCCAGGAG TAGTGGAG GCTTTTTGG AGGCCTAGGC  
GGTACCGACT GATTAAGAA AATAAATAAG TCTCCGGCTC CGGGGGAGCC GGAGACTCGA TAAGGTCTC ATCACTCTC CGAAAAACC TCCGGATCCG

2201 TTTCGAAA AGCTGTAAAC AGCTTGGCAC TGCCCCGTGT TTACACAGT CGTACTGGG AAAACCTGG CGTACCTCAA CTTAATCGCC TTGAGGACA  
AAAACGTTT TCGACAATTG TCGAACCGTG ACCGGCAGCA AAATGTGCA GCACGTGACCC TTGGGAGCC TAAAGGGTT GAATTAGGG AACGTCGTGT

2301 TCCCCCCTTC GCGAGCTGGC GTAAATGGCA AGAGGGCCC ACCGATGCC CTTCCCCAACAA GTTGCCTAGC CTGAATGGGG ATGGGCCCT GATGGGTAT  
AGGGGGAAAG CGGTGCAACCG CATTATCGCT TCTCCGGGG TGCTAGGG GAAGGGTTGT CAACGCATCG GACTTACCGC TTACCGGGAA CTACGCCATA

2401 TTTCCTCTTA CGCATCTGT CGGTATCTCA CACGCCATAC GTCAAAGCAA CCATAGTAGC CGCCCTGTAG CGGGCATTAA AGGGGGGG GTGTGGTGGT  
AAAGAGGAAT GCGTAGACAC GCCATAAAAGT GTGGGTATG CAGTTCTGT GGATCATGC GCGGGACATC GCGGGTAAT TGCGGCCGC CACACACCA

2501 TACGGCAGC GTGACCCGCTA CACTGGCAG CGCCCTAGCG CCGGCTCTT TCGCTTCTT CCGGCTCAGT TCCCGGGCT TCGGCACGT  
ATGGCGCTCG CACTGGCGAT GTGAACGGTC GGGGGATCGC GGGGGATCGC GCGGGACATC GCGGGTAAT TGCGGCCGC CACACACCA

2601 GCTCTAAATC GGGGGCTCCC TTAGGGTTC CGATTAGTG CTTAACGGCA CCTCGACCCC AAAAAACTTG ATTGGGTGA TGTTCACTG AGTGGCCAT  
CGAGATTAG CCCCGAGGG AAATCCAAAG GCTAAATCAC GAAATGGGG TTGGTGAAC TAAACCACT ACCAAGTGCATC TCACCCGGTA

2701 CGCCCTGATA GACGGTTTT CGCCCCTTGCA CGTGGCACTC CACGTTCTTT AATAGTGGAC TCTTGTGTC AACTGGAA CA AACTCAACC CTATCTGGG  
CGGGGACTAT CTGCCAAAAA GCGGGAAACT GCAAACCTAG GTGCAAGAAA TTATCACCTG AGAACAGGT TTGACCTGT TGTGAGTTG GATAAGGCC

2801 CTATTCTTT GATTATAAG GGATTGGCC GATTGGTTAA AAAATGAGCT GATTTAACAA AAATTAACG CGAACATTAA CAAATATTA  
GATAAGAAA CTTAAATATT CCTAAAACGG CTAAGCCGG ATAACCAATT TTACTCGA CTAATGTT TTAAATTGC GCTTAATT GTTTATAT

2901 ACGTTTACAA TTATGGTG CACTCTCACT ACAATCTGCT CTGATGGCC ATAGTTAACG CAACTCCGCT ATCGCTACGT GACTGGGTCA TGGCTGGCC  
TGCCTAACATGTT AAAATACAC GTGAGAGTC TGTAGACCA GACTACGGC TATCAATTGCG GTTGAAGCGA TAGGATGCA CTGACCCAGT ACCGACGGG

3001 CCGACACCCG CCAACACCCG CTGACCGGCC CTGACGGGCT TGTCTGGCTCC CGGCATCCGC TTACAGACAA GCTGTGACCG TCTCCGGAG CTGCATGTT  
GGCTGTGGGC GGTGTGGGC GACTGGGG GACTGGGG GACTGGGG GACTGGGG GCGTAGGGC AATGTCGTT CGACACTGGC AGAGGCCCTC GACGTACACA

3101 CAGGGTTT CACCGTCAT ACCGAAACGC GCGAGGGAGT ATTCTTGAG ACAGAAAGGG CTCGTGATAC GCCTATTGTT ATAGGTTAAT GTCATGATAA  
GTCTCCAAA GTGGCACTAG TGGCTTGCG CGCTCCGTCA TAAGAACCTC TGCTTCCCG GAGCACTATG CGGATTTAATACAA TATCCAAATT CAGTACTATT

3201 TAATGGTTTC TTAGACGTC GGTGGCACTT TTCGGGGAA TGTGGGGGA ACCCCATTGTT GTTATTGTT CTAAATACAT TCAATATGT ATCCGGTCA  
ATTACCAAG AATCTGCACT CCACCGTGA AAGCCCTTT ACACGGCCCT TGGGATAAA CAAATAAA GATTATGTA AGTTTATAACA TAGGGAGTA

3301 GAGACATAA CCTCTGATAAA TGCTTCATAA ATTGTGAAA AGGAAGAGTA TGAGTTATCA ACATTCGGT GTGCCCTTA TTCCCTTT TGCGGATT  
CTCTGTATT GGGACTATT AGGAAGTTT TATAACTTT TCCTCTCAT ACTATAAGT TGTAAGGCA CAGGGAAAT AAGGGAAAAA ACGGCCAAA

3401 TGCCCTTCCTG TTTCGCTCA CCCAGAAACG CTGGTGAAG TAAAGATGC TGAGATCAG TGGGGCAC GAGTGGCTA CATCGAACTG GATCTAAACA  
ACGGAAAGGAC AAAAACGAT GGGTCTACG ACTTCTACG AACCCACGTG CTCACCCAT GTAGCTGAC CTAGACTGT

3501 GCGGTAAGAT CCTTGAGGT TTTCGCCCCG AAGAACGTTT TCCAAATGATG ACCCTTTA AAGTCTGCT ATGTTGCG GTTATTATCCC GTGATGACGC  
CGCCATTCTA GMAACTCTCA AAAGCGGGC TTCTTGCAA AGGTACTAC TCGTAAAT TTCAAGACGA TACACCGGC CATAATAGGG CACTACTGCG

3601 CGGGCAAGAG CAACTCGGTG GCGCATACAA CTATTCTCAG AATGACTTGG TTGAGTACTC ACCAGTCACA GAAAGGATC TIAACGGATGG CATGACAGTA  
GCCCGTTCTC GTTGAAGGCAG CGCGTATGT GATAAGAGTC TTACTGAACT AACTCATGAG TGGTCAGTT GTTTCGTTG AAATGCTTACG GTACTGTCTA

3701 AGAGAATTAT GCAGTGTGC CATAACCATG AGTGATAACA CTGGGCCAA CTTACTTCCTG ACAACGATCG GAGGCCGA GGAGCTAACCGT GCTTTTTGC  
 TCTCTTAATA CGTCACCGACG GTATTGGTAC TCACTATTGT GACGCCGTT GATGAAAGAC TGTGCTAGC CCTCTGGCTT CCTCGATTGG CGAAAAAACG  
 3801 ACAACATGGG GGATCATGTA ACTCGCCTTG ATCGTGGGA ACCGGAGCTG AATGAAGCCA TACCAACGA CGAGCGTGC ACCACGATGC CAGCAGCAAT  
 TGTGTACCC CCTAGTACAT TGAGCGAAC TAGCAACCT TGGCCTCGAC TTACTTGGT ATGTTTGGT GCTCGACTG TGGTGTACG GTCTCGTTA  
 3901 GGCAACAAAC TTGGCCAAAC TATTAACCTGG CGAACTACTT ACTCTAGCTT CCCGCAACA ATTAATAGAC TGGATGGAG CGGATAAGT TGCAGGACCA  
 CGGTGTGTC AACCGGTTTG ATAATGACC GCTGTGAA TGAGATCGAA GGGCGTTGT TAATTATCTG ACCTACCTCC GCCTATTCA ACGTCTGGT  
 4001 CTTCTGGCT CGGCCCTTC GGCTGGCTGG TTATGGCTG ATAAATCTGG AGCCGGTGTAG CGTGGCTTC GGGTATCAT TCCAGGACTG GGGCGAGATG  
 GAAGAGCGGA GCGGGAAAGG CCGACCGACC AAATAACGAC TATTTAGACC TGGCCACTC GCACCCAGAG CGCCATAGTA ACGTCCTGAC CCCGGTCTAC  
 4101 GTAAAGCCCTC CGGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT ATGGATGAAC GAAATAGACA GATCGCTGAG ATAGGTGCT CACTGATAA  
 CATTGGGAG GGCATAGCAT CAATAGATGT GCTGGCCCTC AGTCGGTGA TACCTACTTG CTTTATCTGT CTAGGGACTC TATCCACGGA GTGACTAATT  
 4201 GCATTGGTAA CTGTCAGACC AAGTTTACTC ATATATACTT TAGATTGATT TAAACCTCA TTTTTAATT AAAAGGACTT AGGTGAAGAT CCTTTTGAT  
 CGTAACATT GACAGTCTGG TTCAAAATGAG TATATATGAA ATCTAACTAA ATTGTGAAGT AAAAATTAAA TTTCTAGA TCCACTCTA GGAAAAACTA  
 4301 AATCTCATGA CCAAAATCCC TAAACGTGAG TTTCTGTCC ACTGAGGCTC AGACCCCTA GAAAGATCA AAGGATCTC TTGAGATCCT TTTTTCTGC  
 TTAGAGTACT GGTTTAGGG AATTGCACTC AAAAGCAAGG TCACTCGCAG TCTGGCCAT CTTTCTGT TTCTAGAAG AACTCTAGGA AAAAGACG  
 4401 GCGTAATCTG CTGCTTGCAA ACAAAAC CACCGCTTACG AGCCGGTGTAG TGTGTGCGG ATCAAGAGCTT ACCAAGCTT TTCCGAAGG TAACTGGCTT  
 CGCATTAGAC GACGAACGTT TGTGTTTGTG GTGGCGATGG TCGCCACCAA ACAAACGGCC TAGTTCTCGA TGGTTGAGAA AAAGGCTTC ATTGACCGAA  
 4501 CAGCAGAGCG CAGATAACCA ATACTGTCTT TCTAGTGTAG CGTAGTGTAG GCCACCACTT CAAGAACTCT GTAGCACCGC CTACATACCT CGCTCTGCTA  
 GTCGTCTCGC GTCTATGTT TATGACAGGA AGATCACATC GGCAATCATC CGGTGGTGA GTTCTTGAGA CATCGTGGCG GATGTATGGA GCGAGACGAT  
 4601 ATCCTGTAC CAGGGCTGC TGCCAGTGGC GATAAGTGTAG GTCTTACGGG GTTGGACTCA AGACGATAGT TACCGGATAA GGCGAGCGG TCGGGCTGAA  
 TAGGACATG GTCAACCGACG ACGGTCAACCG CTATCAGCA CAGAATGGCC CAACCTGAGT TCTGCTATCA ATGGCCATT CGCGTGCCTT AGCCCGACTT

4701 CGGGGGTTIC GTGCCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA CTGAGATACC TACAGCGTGA GCATTGAGAA AGGCCACGG AGGCCAAGG  
 'GCCGCCAAG CACGTGTGTC GGTCGAACC TCGCTTGTG GATGTGGCTT GACTCTATGG ATGTCGCACT CGTACTCTT TCGGGTGC AAGGGCTTCC  
 4801 GAGAAAGGG GACAGGTATC CGGTAAAGGG CAGGGTGGG ACAGGGAGGC GCACGGAGG GCTTCCAGGG GAAAACGGCT GGTTATCTTTA TAGTCTGTC  
 CTCTTCCGC CTGTCCATAG GCCATTGCGC GTCCCCAGCCT TGTCCCTCG CGTGTCCCT CGAAGGTTCC CCTTGGGAA CCATAGAAAT ATCAGGACAG  
 4901 GGGTTTCGCC ACTCTGTACT TGAGCGTCA TGAGCGTCACTGTTT GCTCGTCAAG GGGGGGAGC CTATGGAAAA AGCGCAGCAA CGGGGCTT TTACGGTCC  
 CCCAAAGGG TGAGGACTGA ACTCGGACCT AAAAACACTA CGAGGAGTCC CCCGGCTCG GATAACCTTT TGCGGTGTT GGCGGGAAA AATGCCAAGG  
 5001 TGGCCTTTTG CTGGCCTTTT GCTCACATGT TCTTTCCTGC GTTATCCCTT GATTCCTGTGG ATAAACCGTAT TACGCCCTT GAGTGGCTG ATACCGCTCG  
 ACCGGAAAC GACCGGAAA CGAGTGTACA AGAAAGGACG CAATAGGGAA CTAAGACACC TATGGCATA ATGGGGAAA CTCACTCGAC TATGGGAGC  
 5101 CCGCAGCCGA ACGACCGAGC GCAGCGAGTC AGTCAAGGGAG GAAGCGGAAG AGCGCCCAAT AGCGAACCCG CCTCTCCCC CGCGTGGCC GATTCACTAA  
 GGGGTGGCTT TGCCTGGCTCG CGTCTGGCTCA TCACTCGCTC CTTGGCCTTC TCGGGGTTA TGCGTTGGC GGAGGGGG CGCAACCCG CTAAGTAATT  
 5201 TCCAGCTGGC ACGACAGGTT TCCCGACTGG AAAGCGGGCA GTGAGCGCAA CGCZATTAAAT GTGAGTTAAC TCACTCAATT GGCACCCAG GCTTTACACT  
 AGGTGACCG TGCCTGTCAA AGGGCTGACC TTTGGCCGT CACTCGCTT GCGTTAATTAA CACTCAATTG AGTCAATT CCGTGGGGTC CGAAATGTGA  
 5301 TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGGG AAACAAATT CACACAGGA ACAGCTATGA CCATGATTAC GAATTAA  
 AATACGAAGG CCGAGGCATAC AACACACTT AACACTCGCC TATTGTTAAA GTGTGCTT TGTGCTACTT GTGACTAATG CTTAATT

FIG.- 33 F

1 ATTGGAGCTC GCCCCGACATT GATTATTGAC TAGTTATCAA TAGTATCAA TACGGGGTC ATTAGTTCAT AGCCCCATA TGGAGTTCCG CGTTACATAA  
 TAAGCTGAG CGGGCTGAA CTAATACTG ATCAATAATT ATCATATTGTT AATGCCCCAG TAATCAAGTA TCGGGTATAT ACCTCAAGGC GCAATGTTATT  
  
 101 CTTACGGTAA ATGGCCGCC TGGCTGACCG CCCAACGACC CCCGCCATT GACGTCAATA ATGACGTATG TTCCCATAGT AACGCCATA GGGACTTCC  
 GAATGCCATT TACCGGGGG ACCGACTGGC GGGTGTGG GGGGGGTTAA CTGCAAGTTAT TACTGCATA AAGGGTATCA TTGCGGTAT CCCTGAAAGG  
  
 201 ATTGACGTCA ATGGTGGAG TATTACGGT AACTGCCCA CTGGGAGTA CATCAAGTGT ATCATATGCC AAGTACGCC CCTATTGACG TCAATGACGG  
 TAACTGCACTG TACCCACCTC ATAAATGCCA TTGACGGGT GAAACCGTCAT GTAGTTCAAA TAGTATACGG TTCAATGCC AGTTACTGCC  
  
 301 TAAATGGCCC GCCTGGCATT ATGCCAGTA CATGACCTTA TGGGACTTTC CTACTGGCA GTACATCTAC GTATTAGTCAT CGTGTATAC  
 ATTACCGGG CGGACCGTA TACGGTCAAT GTACTGGAAT ACCCTGAAAG GATGAACCGT CATGTAGATG CATAATCAGT AGCGATAATG GTACCACTAC  
  
 401 CGGTITGGC AGTACATCAA TGGCGTGGAA TAGCGGTTTG ACTCACGGG ATTTCAGT CTCCACCCCA TTGACGTCAA TGGGAGTTTG TTGGCACC  
 GCCAAACCG TCACTGACTT ACCCGCACCT ATGCCAAAC TGAGTGCCTCA GAGGTGGGT AACTCAGTT ACCCTCAAAAC AAAACCGTGG  
  
 501 AAAATCAACG GCACTTTCCA AAATGTCGTA ACAACTCCGC CCCATTGACG CAATGGCG GTAGGCCTGT ACGGTGGAG GTCTATATAA GGAGAGCTCG  
 TTTTATGTTGC CCTGAAGGT TTACAGCAT TTGTTGAGGG ACATAACTGG GGGTAACCTGC GTTACCCGC CATCCGCACA TGCCACCCCT CAGATATATT CGTCTCGAGC  
  
 601 TTAGTGAAC CGTCAGATCG CCTGGAGACG CCATCCACGC TGTTTGACCC TCCATAGAAG ACACCCGGAC CGATCCAGCC TCCGGGGCG GGAACGGTGC  
 AAATCACTTG CGAGCTCTAG GGACCTCTGC GGTTGGGTGGC ACAAAACTGG AGGTATCTTC TGTGGCCCTG GCTAGGTGG AGGGCCGGC CCTTGCCACG  
  
 701 ATTGGAACGC GGATTCCCG TGCCAAAGCT GACGTAAGTA CCGCCTATAG AGTCTATAGG CCCACCCCT TGGCTTCGTT AGAACGGGGC TACAATTAAT  
 TAACCTTGGC CCTAAGGGGC ACGGTTCAC CTGCACTCAT GGGGGATATC TCAGATATCC GGGTGGGGAA ACCGAAAGCAA TCTTGGCCCG ATGTTAATTA  
  
 801 ACATAACCTT ATGTATCAA CACATAGAT TTAGGTGACA CTATAGAATA ACATCCACTT TGCTTCTC TCCACAGGTG TCCACTCCCA GGTCCAACGT  
 TGTATGGAA TACATAGAT GTGTATGCTA AATCCACTGT GATATCTAT TTGAGGTGAA ACGGAAAGAG AGGTGTCCAC AGGTGAGGGT CCAGGGTGC  
  
 901 CACCTCGGTT CTATCGATTG AATTCCACCA TGGGATGGTC ATGTATCATT CTTTTCTAG TAGCAACTGC AACTGGAGCG TACGCTGAGG TTCAGCTGGT  
 GTGGAGCCAA GATAGCTAAC TTAGGTGGT ACCCTACCAAG TACATAGTAG GAAAAGATC ATCGTTGACG TTGACCTCGC ATGGGACTCC AAGTCGACCA

1

M G W S C I I L F L V A T A T G A Y A E V Q L V  
 ^start signal peptide  
 ^met  
 ^start of heavy chain  
 ^BsiWI

FIG. - 34A

1001 GGAGTCTGGC GTGGCCTGG TGCAGCCAGG GGGCTCACTC CGGCTTGTCTC GGCAGCTTC TGGCTTACCC ATTAGTGGT CTTGGGATACA CTGGGTGCGT  
 25 E S G G G L V Q P G G S L R L S C A A S G F T I S G S W I H W V R  
 ^CDR-H1

1101 CAGGCCCGG GAAAGGGCCT GGAATGGGT GCTTGGATTG CTCCTTATAG CGGGCGTACT GACTATGCCG ATAGCGTCAA GGGGCGTTTC ACTATAAGCG  
 GTCCGGGCC CATTCCGGA CCTTACCCAA CGAACCTAAC GAGGAATATC GCCGGCATGA CTGATAACGGC TATGCCAGTT CCGGCAAG TGATATTGCG  
 58 Q A P G K G L E W V A W I A P Y S G A T D Y A D S V K G R F T I S A  
 ^CDR-H2

1201 CAGACACATC CAAAAACACA GCCTAACCTAC AAATGAACAG CTTAAGAGCT GAGGACACTG CGGTCTTATA TTGTTGCAAGA GAGGGGGCT TGTACTGGGT  
 GTCTGTAG GTTTTGTGT CGGATGGATG TTACTTGTCTC GAATTCTCGA CTCTGTGAC GGAGATAAT AACACGTCTC CTCCCCCGA ACATGACCCA  
 92 D T S K N T A Y L Q M N S L R A E D T A V Y Y C A R E G L Y W V  
 ^CDR-H3

1301 GTTCGACTAC TGGGGTCAAG GAACCCCTGGT CACCGCTCTCC TCGGCCCTCCA CCAAGGGCCC ATCGGGTCTTC CCCCTGGCAC CCTCCTCCAA GAGCACCTCT  
 CAAGCTGTAG ACCCCAGTTC CTGGGGTGG ACCGGGAGGG AGGGGGAGGT GGTGAGGGT GGTCGGGGGG TAGCCAGGA GGGGACCGTG GGAGGGGGTT CTCGGGGAGA  
 125 F D Y W G Q G T L V T V S S A S T K G P S V F P L A P S S K S T S  
 ^Apal

1401 GGGGCACAG CGGCCCTGGG CTGCCCTGGTC AAGGACTACT TCCCCGAACC GGTGAGGGT TCGTGGAACT CAGGGCCCT GACCAGGGC GTGCACACCT  
 CCCCCGTGTC GCGGGGACCC GACGGGACCA GACGGGACAG TTCCCTGTATGA AGGGGGCTGG CCACCTGCTGA AGCCACCTGA GTCCGGGGGA CTGGTGGCG CACGTTGGA  
 158 G G T A A L G C L V K D Y F P E P V T V S W N S G A L T S G V H T F

1501 TCCCCGGTGT CCTACAGTTC TCAGGACTCT ACTCCCTCAG CAGGGCTGGTG ACTGTGGCCTT CTAGGAGCTT GGGCACCCAG ACCTACATCT GCAAGCTGAA  
 AGGGCCGACA GGATGTCAAG AGTCCTGAGA TGAGGGAGTC GTCGCACCA TGACACGGGA GATCGTCAA CCCGGGGCTC TGGATGTAGA CGTTCCACTT  
 192 P A V L Q S S G L Y S L S V V T V P S S L G T Q T Y I C N V N

1601 TCACAAAGCCC AGAAACACCA AGGTGGACAA GAAAGTTGAG CCCAAATCTT GTGACAAAAAC TCACACATGC CCACCGTGGCC CAGCACCTGA ACTCCCTGGGG  
 AGTGTGTGGG TCGTGTGGT TCCACCTGTT CTTCACACTC GGGTTTAA CACTGTTTG AGTGTGTAGG GGTGGCAGGG GTCTGGAACT TGAGGACCC

225 H K P S N T K V D K K V E P K S C D K T H T C P P C P A P E L L G

1701 GGACCGTCAG TCTTCCCTCTT CCCCCAAA CCAAGACA CCTCCGACC CCTGAGGTCA CATGGTGGT GTGGACGTG AGCCACCGAAG  
 CCTGGCAGTC AGAAGGAGAA GGGGCTTT GGGGCTCTGT GGACTCAGT GTACGCCCA CCACCTGCAC TCGGTGCTTC  
 258 G P S V F L F P P K P K D T L M I S R T P E V T C V V V D V S H E D

1801 ACCCTGAGGT CAAGTCAAC TGGTACGTGG AGGGCCTGG AGGTGCATAAT GCAAGACAA AGCCGGGGAA GGAGCACTAC AACAGCACGT ACCGGGTGGT  
 TGGGACTCCA GTTCAAGTGT ACCATGCC ACCATGCC TGGTCTGTGC CGACTTACCG TCCCTCATGT TCACTGTCCA GAGGTGGT CTTTGGTAG  
 292 P E V K F N W Y V D G V E V H N A K T K P R E E O Y N S T Y R V V

1901 CAGCGTCCTC ACCGGACTG GCTGAATGGC AAGGAGTACA AGTCCAAGGT CTCCAAACAA GCCTCCAG CCCCATCGA GAAACCATC  
 GTCGCAGGAG TGGCAGGAG CGACTTACCG TGGTCTGTGC CGACTTACCG TCCCTCATGT TCACTGTCCA GAGGTGGT CTTTGGTAG  
 325 S V L T V L H Q D W L N G K E Y K C K V S N K A L P A P I E K T I

2001 TCCAAGCCA AAGGGCAGCC CCGAGAACCA CAGGTGTACA CCTGCCCCC ATCCGGAA GAGATGACCA AGAACAGGT CAGCCTGAC TGCCTGGCA  
 AGGTTTCGGT TCCCCGGTGG GGCTCTGGT GTCCACATGT GGACACCTT TAGGGCCCTT CTCTACTGGT TCTGGTCCA GTGGACTGG ACGGACCAAGT  
 358 S K A K G Q P R E P Q V Y T L P P S R E E M T K N Q V S L T C L V K

2101 AAGGGCTTCTA TCCAGGCAC ATGCCCTGG AGGGAGAG CAAATGGCAG CGGAGAAC ACTACAAAC CACGCCCTCC GTGCTGGACT CGGACGGTC  
 TCCGGAAAGT AGGGCTGGTAGGGCTCTC TCACCCCTCTC GTTACCGTC GGCTCTGT TGATGGTCTGT GTGGGGAGGG CACGACCTGA GGCTGCCAG  
 392 G F Y P S D I A V E W E S N G O P E N N Y K T T P P V L D S D G S

2201 CCTCTTCCTC TACAGCAAGC TCACAGGCAC TGGCAGGAGG GGAACGTCTT CTCACTGCTCC GTGATGGCATG AGGCTCTGCA CAACCACTAC  
 GAAGAGGGAG ATGTCGGTGG AGTGGCACCT GTTCTCGTCC ACCGTCCTCC CCTTGAGAA GACTACGAGG CACTACGTAC TCCGAGACGT GTGGTGTAG  
 425 F F L Y S K L T V D K S R W Q Q G N V F S C S V M H E A L H N H Y

2301 ACGCAGAAGA GCCTCCCT GTCTCCGGT AATGAGTGC GACGCCCTA GAGTCGACCT GCAGAACCTT GGCGCCATG GCCAACACTG TTTATGGAG  
 TGGGTCTCTC CGGAGAGGA CAGAGGGCA TTTACTCAG CTGCCGGAT CTCAAGTGGAA CGTCTCGAA GTGACGTAAC CGGGGGTAC AAATAACGTC  
 458 T Q K S L S I S P G K O

2401 CTTATAATGG TTACAAATAA AGCAATAGCA TCACAAATT CACAATAAA GCATTTT CACTGCATTC TAGTTGTGGT TTGTCAAAC TCATCAATGT  
 GAATATACCA ATGTTTATT TCGTTATCGT AGTGTAA GTGTTTATT CGTAAAAA GTGACGTAAG ATCACACCA AACAGGTTTG AGTACCTACA

2501 ATCTTATCAT GTCGGATCG ATCGGAATT AATCGGCC AGCACCATGG CCTGAAATAA CCTCTGGAAAG AGGAACATGG TTAGGTACCT TCTGAGGGGG  
TAAATAAGTA CAGACCTAGC TAGGCCCTAA TTAAGCCGG TCCTGGTACCG GGAATTGGTACCT GGAGACTTTC TCCTTGAACC AATCCATGGA AGACTCCGCC  
2601 AAAGAACCAT CTGTGGAAATG TGTGTCAAGTT AGGGTGTGGAA AAGTCCCAG GCTCCCCAG AGGCAGAAAGT ATGCAAAGCA TGCATCTAA TTAGTCAGCA  
TTTCTGGTA GACACCTAAC ACACAGTCAC TCCCACACCT TTCAAGGGTACCT CGAGGGTGC CGAGGGTGC TCCGGTCTCA TACGTTTCGT ACGTAGAGTT AATCAGTCGT  
2701 ACCAGGTGTG GAAAGTCCCC AGGCTCCCCA GCAAGGCAAA GTATGCAAAG CATGCATCTC AATTAGTCAG CAACCATAGT CCCGCCCTA ACTCCGCCCA  
TGGTCACAC CTTCTAGGGG TCCGGGGGT CGTCCGGTCTT CATACTTTC GTACGTAGAG TTAATCAGTC GTTGGTATCA GGGGGGGAT TGAGGGGGT  
2801 TCCCGCCCT AACTCCGGCC AGTTCCGGCC ATTCCTCCGCC CCATGGCTGA CTAATTTCCTT TTATTATGC AGAGGCCAG GCGCCCTCGG CCTCTGAGCT  
AGGGGGGGAA TTGAGGGGGG TCAAGGGGGG TAAGAGGGGG GGTACCGACT GATTAaaaaaa AATAAATACG TCTCCGGCTC CGGGGGAGCC GGAGACTCGA  
2901 ATTCCAGAAG TAGTGGAGG GCTTTGG AGGCCTAGGG TTTTGCAGCA TCCCCTTC GCCAGTTGGC AGCTTGGCAC AGGGCCGAG TGGCCGTGTT TTACAAAGT  
TAAGGGCTTC ATCACTCCTC CGAAAACC TCGGGATCCG AAAACGTTT TCGACAATTG TCGAACCTGT ACCGGCAGCA AAATGTTGCA GCACTGACCC  
3001 AAAACCTGG CGTTACCCAA CTTAATCGCC TTGAGGCACA TCCCCTTC AGCTGTTAAC AGCTTGGCAC TGGCCGTGTT AGCTGGCC ACCGATGCC  
TTTGGGACC GCAATGGGT GAATTGGGG AACGTCTGT AGGGGGAAAG CGGTCAACCG CATTATGCT TCTCCGGCG TGGCTAGCGG GAAGGGTTG  
3101 GTTGGCTAGC CTGAATGGCG AATGGGCCT GATGGGGTAT TTTCTCCTTA CGCATCTGT CGGTATTCTCA CACCGCATA GTCAAAGCAA CCATAGTACG  
CAACGGATCG GACTTACCGC TTACCGGGCA CTACGCCATA AAAGGAAAT GGTAGACAC GCCATAAAGT GTGGCTATG CAGTTTCGTT GGTATCATGC  
3201 CGCCCTGTAG CGGGCATTAA AGGGCGGG GTGTGGTGGT TACGGGAGC GTGACCGCTA CACTGGCAG CGCCCTAGGC CGCGCTCCCT TCGCTTTCTT  
CGGGGACATC GCGCGTAAAT TCGGGCGCC CACACCAAA ATGGCGTGC CACTGGGAT GTGAACGGTC GGGGATCGC GGGCAGGGAA AGGGAAAGAA  
3301 CCCTTCTTT CTGGCCACGT TCGCCGGCTT TCCCGGTCAA GCTCTAAATC GGGGGCTCCC TTAGGGTTC CGATTAGTC CTTTACGGCA CCTCGACCC  
GGGAAGGAAA GAGGGGTGCA AGGGGGCGAA AGGGGGAGTT CGAGATTAG CCCCCGAGGG AAATCCIAAG GCTAAATCAC GAAATGGCGT GGAGCTGGGG  
3401 AAAAAACTTG ATTGGGTGA TGGTTCACTG AGTGGCCAT CGCCCTGATA GACGGTTTTGA CGCCCTTGTCA CGCTTACGGCA CCTCGACCC  
TTTGTGAAC TAAACCCACT ACCAAGTGGCA TCACCCGGTA GGGGGACTAT CTGCCAAAAA GCGGGAAACT GCAACCTCAG GTGCAAGAAA TTATCACCTG

3501 TCTTGGTCCA AACTGGAACA AACTCAACC CTATCTGGG CTATTCTTT GATTTAAG GGATTTGCC GATTTCGGCC TATTGGTAA AAAATGAGCT  
 AGAACAGGT TTGACCTTGT TGTGAGTTGG GATAGGCC GATAAGAAA CCTAAATTC CCTAAACGG CTAAGCCG ATAACCAATT TTTTACTCGA  
 3601 GATTAAACAA AAATTAAACG CGAATTAAACAA CAAATATTAA ACGTTTACAA TTATGGTG CACTCTAGT ACAATCTGGT CTGATGCCG ATAGTTAACG  
 CTAATGTT TTAAATTGC GCTTAATT GTTTATAAT TGCAATGTT AAAATACCA CTGAGAGCA TGTAGACGA GACTACGGG TATCAATTGCG  
 3701 CAACTCGGCT ATCGCTACGT GACTGGTCA TGGCTGGCC CCGCACCCG CCAACACCCG CTGACCGGCC CTGACGGGCT TGTCTGCTCC CGGCATCCGC  
 GTTGAGGCGA TAGCGATGCA CTGACCACT ACGGACGGG GGCTGTGGC GGTGTGGG GACTGGGG GACTGCCGA ACAGACGAGG GCCGTAGGG  
 3801 TTACAGACAA GCTGTGACCG TCTCCGGAG CTGGCATGTT CAGAGGTTT CACCGTCATC ACCGAAACGC CGGAGGCACT ATTCTGAAG ACGAAGGGC  
 AATGCTGTT CGACACTGGC AGAGCCCTC GACGTACACA GTCTCCAAA GTGGCAGTAG TGCTCCGTCA TAAGAACTTC TGCTTCCCG  
 3901 CTCGTGATAC GCCTATTGTT ATAGGTTAAT GTCATGATAA TAATGGTTTC TTAGACGTCA GGTGGCACTT TTGCGGGAAA TGTCGGGAA ACCCCATT  
 GAGCACTATG CGGATAAAA TATCCATTAA CAGTACTATT ATTACCAAAG AATCTGGAGT CCACCGTGA AAGCCCCTT ACACGGCCT TGCGGATAAA  
 4001 GTTTATTTT CTAATAACAT TCAATAATGT ATCGCTCAT GAGACAATAA CCCTGATAAA TGCTTCATAA ATATTGAAA AGGAAGAGTA TGAGTATTCA  
 CAAATAAAA GATTATGTA AGTTATACA TAGGCGAGTA CTCGTATT GGGCACTATT ACCAAGTTT TATAACFTT TCCTTCTCAT ACTCATAGT  
 4101 ACATTTCGGT GTGCCCTTAA TTCCCTTTTG CGGGCATTT TGCCCTTCCTG TTTTGCTCA CCCAGAAACG CTGGTAAAG TAAAGATGC TGAAGATCAG  
 TGTAAGGCA CAGCGGGAAAT AAGGAAAAA ACGGCGTAA ACGGAAGAC AAAAACGAGT GGGCCTTTC GACCACTTC ATTTCCTACG ACTTCTAGTC  
 4201 TTGGGTGCAC GAGTGGTTA CATGAACTG GATCTCAACA GCGGTAAGAT CCTTGAGAGT TTTGCCCG AAGAACGTT TCCAATGAG AGCACTTTA  
 AACCCACGTG CTCACCCAAAT GTAGCTTACG CTAGAGTTGT CGCCATTCTCA GGAACCTCTCA AAAGGGGGC TTCTTGCAAA AGGTACTAC TCCTGAAT  
 4301 AAGTTCTGCT ATGTGGCGG GTTATTACCC GTGATGACGC CGGGCAAGAG CAACTCGGTG GCCGCATACA CTATTCCTAG ATGACTTGG TTGAGTACTC  
 TTCAAGACGA TACACCGGC CATAATGGG CACTACTGGG GCGCGTTTC GTCGAGCCAG CCCGTTCTC GGGGTATGT GATAAGAGTC TAACTCATGAG  
 4401 ACCAGTCACA GAAAGCATTCA TTACGGATGG CATGACAGTA AGAGAATTAT GCAAGTAAACA CTTACTATGT GACTATGGTAC TCACTATTGT GACTATGAG  
 TGGTCAGTGT CTTTCGTAG AATGCCCTACC GTACTCTCAT TCTCTTAACTA CGTCAGCAGCG GTATGGTAC CTTACTCTGTT GAAATGAGAC  
 4501 ACAACGATCG GAGGACCGAA GGAGCTAACG GCTTTTGC ACAACATGGG GGATCATGTA ACTCGCCTTG ATCGTGGGG ACGGGAGCTG AATGAGGAA  
 TGGTGTAGC CTCTGGCTT CCTCGATGG CGAAAAACG TGTGTACCC CCTAGTACAT TAGGGAAAC TAGCAACCT TAGGCGCTGAC TTACTTCCGT

4601 TACCAAACGA CGAGCGTGC ACCACCATGC CAGCAGCAAT GGCAACAAAG TTGCGAAAC TATTAACCTGG CGAACTACTT ACTCTAGCTT CCCGGCAACA  
 ATGGTTTGCT GCTCGACTG TGGTGTCTAGC GTCTGCTGTTA CCGGTGTGTC AACGGCTTTCG ATAAATGACC GCTGTGAA TGAGATGAA GGGCGTGT  
 4701 ATTAATAGAC TGGATGGGG CGGATAAGT TGCAGGACCA CTTCCTGGCT CGGCCCTTC GGCTGGTGG TTATATGCTG ATAAATCTGG AGCCGGTGA  
 TAATTAATCTG ACTAACCTTC GCCTATTTCA ACGTCTCTGGT GAAGACCGGA GCGGGAGG CGAACCGACC AAATAACGAC TATTTAGACC TGGCCACT  
 4801 CGTGGCTCTC GCGGTATCAT TGCAGGACTG GGGCCAGATG GTAAAGCCCTC CCGTATCGTA GTATCTACA CGACGGGAG TCAAGGCAACT ATGGATGAA  
 GCACCCAGAG CGCCATAGTA ACGTCTGTAC CCCGGCTAC CATTGGGAG GGCAATAGCAT CAATAGATGT GCTGCCCTC AGTCCGTTGA TACCTACTTG  
 4901 GAAATAGACA GATCGCTGAG ATAGGGCCT CACTGATTAA GCATTGGTAA CTGTCAGACC AAGTTACTC ATATATACTT TAGATGATT TAAACTCTA  
 CTTTATCTGT CTAGCGACTC TATCCACGGA GTGACTAATT CGTAACATT GACAGCTGG TTCAAAATGAG TATATATGAA ATCTAACTAA ATTTGAAGT  
 5001 TTTTTAATT AAAAGGATCT AGGTGAAGAT CCTTTTGAT AATCTCATGA CCAAATCCC TTAACTGTAG TTTTGTCC ACTGAGCGTC AGACCCCGTA  
 AAAAATAAA TTTTCCTAGA TCCACTCTA GGAAAACAA TTAGAGTACT GGTTTGGG ATTTGACTC AAAAGCAAGG TGAATCGCAG TCTGGGCAT  
 5101 GAAAAGATCA AAGGATCTTC TTGAGATCCT TTTTCTGC GCGTAATCTG CTGCTTGCAA ACAAAAAAC CACCGCTACC AGCGGTGGTT TGTTGGCGG  
 CTTTCTAGT TTCTAGAAG AACTCTAGGA AAAAAGACG CGCAATTAGAC GACGAACGTT TGTTTTTTG GTGGCATGG TCGCCACAA ACAAACGGCC  
 5201 ATCAAGGAGCT ACCAACTCTT TTTCGAAAGG TAACTGGCTT CAGCAGGG CAGATACCAA ATACTGTCTCT TCTAGTGTAG CCCTAGTTAG GCCACACTT  
 TAGTTCTCGA TGGTGAGAA AAAGGCTTCC ATTGACCGAA GTCTGTCTGG GTCTATGGTT TATGACAGGA AGATCACATC GGATCAATC CGGTGGTGA  
 5301 CAAGAACTCT GTAGCACCGC CTACATACCT CGCTCTGCTA ATCCTGTAC CAGTGGCTGC TGCAGTGGC GATAAGTGT GTCTTACGG GTGGACTCA  
 GTTCTTGAGA CATCGTGGG GATGTATGGA GCGGAGCGAT TAGGACATG GTCAACCGAG ACCGTCACCG CTATTCAGCA CAGAATGGCC CAACCTGAGT  
 5401 AGACGATAGT TACCGGATAA GGGCAGGG TCGGGCTGAA CGGGGGTTC GTGCAACACAG CCCAGCTGG AGCGAACGAC CTACACCGAA CTGAGATACC  
 TCTGCTATCA ATGGCCTATT CGCGCTGCC AGCCGACTT GCGCACTGGTGC CACCCCCAAG CACGTGTGTC GGTCAGGCTGCTG GATGTGGCTT GACTCTATGG  
 5501 TACAGGGTGA GCATGTGAGAA AGGCCACGC TTCCGAAAGG GAGAAAGGGC GACAGGTATC CGGTAAAGGG CAGGGTGGAA ACAGGAGGCC GCACGAGGG  
 ATGTGCGACT CGTAACCTT TCGGGTGG AAGGGCTTCC CTCCTTCGGC CTGTCATAG GCCATTGGC GTCCAGGCT TGTCTCTCG CGTGTCTCC  
 5601 GCTTCCAGGG GGAAACGGCT GGTATCTTAA TAGTCTGTCTGG ACCTCTGTC GGGTTTCGGC ACCTCTGACT TGAGCGTCAAG TTTTTGTGAT GCTCGTCAAG  
 CGAAGGTCTCC CCTTGTGGGA CCATAGAAAT ATCAGGACAG CCCAAAGGG TGGAGACTGA ACTCGCAGCT AAAACACTA CGAGCAGTCC CCCCGCTCG

5701 CTATGGAAA AGGCCAGCAA CGGGGCCCTT TTACGGCTTCC TGGCCTTTG CTGGCCTTTT GCTCACATGT TCTTCTCTGC GTTATCCCT GATTCTGTGG  
 GATACTCTTT TGCCTGTGTT GCGCCGGAAA ATGCCAAGG ACCGGAAA CGAGGTACA AGAAGGACG CAATAGGGA CTAAGACACC  
 5801 ATAACCGTAT TACCGCCTT GAGTGAAGCTG ATACCGCTCG CCGCAGCCGA ACGACCGAGC GCAGCGAGTC AGTGAAGCAG GAAGGGAAAG AGC GCCCAAT  
 TATTGGCATA ATGGGGAAA CTCACTCGAC TATGGCAGC TGCTGGCTCG CGTGGCTAG TCACTCGCTC CTTCCGCCTC CGTGGCTTA  
 5901 ACGCAAACCC CCTCTCCCCG CGCGTGGCC GATTCAATTAA TCCAACCTGGC ACGACAGGTT TCCCGACTGG AAAGGGCA GTGAGGGCAA CGCAATTAA  
 TGGCTGGC GGAGGGGGC GCGCAACCGG CTAAAGTAATT AGGTGAACCG TGCTGTCCAA AGGGCTGACC TTTCCGCCGT CACTCGGTT GCGTTAATTA  
 6001 GTGAGCTTACCTCACTCACTTACACTTGTGCTGTATG TTATGCTTCC GGCTCGTATG TTGTGAGGGG ATAACAAATT CACACAGGA  
 CACTCAATGG AGGTGAGTAAT CCGTGGGTC CGAAATGTGA AATAACGAGG CCGAGCATAACACACCT AACACTCGCC TATTGTTAA GTGTGCTT  
 6101 ACAGCTATGA CCATGATTAC GAATTA  
 TGTCGATACT GGCTACTAATG CTTAAT

FIG.- 34 G

LC Frequency	28	S	N	V	D	G	I	T	L	X
28	511	262	258	186	178	44	39	16	35	
29	1	S	V	G	N	X				
29	612	272	254	192	147	70				
30	S	N	K	G	R	Y	T	D	A	X
30	849	176	169	86	81	63	29	28	17	45
31	S	N	T	R	I	D	K	G	X	
31	676	496	170	47	29	28	25	18	53	
32	Y	N	W	F	S	D	R	X		
32	1055	128	97	77	61	40	25	69		
50	G	A	D	W	K	L	E	S	X	
50	386	341	294	151	116	91	39	30	82	
53	S	N	T	K	I	R	X			
53	545	438	407	41	23	23	58			
91	Y	S	R	A	G	H	X			
91	849	196	169	118	61	41	148			
92	Y	G	N	S	D	L	T	H	I	X
92	362	356	248	193	114	94	64	43	38	91
93	S	N	Q	T	H	G	D	R	X	
93	738	346	117	101	66	51	47	35	112	
94	S	T	W	Y	L	F	A	P	V	
94	386	365	288	172	114	79	46	43	33	
96	L	Y	W	F	I	R	P	X	24	18
96	264	205	176	140	117	115	46	121		

FIG.-35

Residue	Natural Diversity	Diversity < DNA codon	% good	% covering
L1-28	SNVDGI	SNVDGI<RDT>	100%	94%
L1-29	ISVGN	ISVG<RKT>	100%	86%
L1-29		IV<RTT>	100%	56%
L1-30	SNKGRYTDA	SNKGGRTTDAAE<RVW>	92%	93%
L1-31	SNTRIDKG	SNTTRDKGGAAE<RVW>	75%	95%
L1-31		SNTTRIIK<ANW>	100%	94%
L1-32	YNWFSDR	YNFSDATIV<DHT>	55%	88%
L1-32		YFS<THT>	100%	77%
L2-50	GADWKLES	GAWLSV<KBG>	83%	67%
L2-53	SNTKIR	SNT<AVC>	100%	90%
L3-91	YSRAGH	YSAD<KMT>	75%	74%
		YS<TMT>	100%	66%
L3-92	YGNSDLTHI	YNSDTIFAV<DHT>	67%	64%
		YNSDTA<DMC>	83%	62%
L3-93	SNQTHGDR	SNTGDA<RVT>	83%	80%
		SNTDYAFIV<DHT>	44%	76%
L3-94	STWYLFAPVI	STYLFAPVINDH<NHT>	75%	78%
		STYFIN<WHT>	83%	43%
L3-96	LYWFIRP	LYFPHS<YHT>	67%	52%
		LYFIHN<HWT>	67%	58%
		LFI<HTT>	100%	42%
		LLWR<YKG>	100%	47%
		YF<TWT>	100%	29%

FIG.- 36

**Light Chain Designed Diversity**  
**Diversity:  $\sim 2.9 \times 10^9$**

**CDR-L1: diversity  $\sim 7 \times 10^3$**

28	29	30	31	32
RDT	RTT	RVW	RVW	DHT
D	I	D	D	A
G	V	E	E	D
I		G	G	F
N		K	K	I
S		N	N	N
V		S	S	S
		T	T	T
		R	R	V
				Y

**CDR-L2: diversity = 18**

50	53
KBG	AVC
A	N
G	S
L	T
S	
V	
W	

**CDR-L3: diversity  $\sim 2.3 \times 10^4$**

91	92	93	94	96
KMT	DHT	DHT	NHT	YHT
A	A	A	A	F
D	D	D	D	H
S	F	F	F	L
Y	I	I	H	P
	N	N	I	S
	S	S	L	Y
	T	T	N	
	V	V	P	
	Y	Y	S	
			T	
			V	
			Y	

**FIG.-** 37

**Light Chain Designed Diversity**  
**Diversity:  $\sim 6.1 \times 10^8$**

**CDR-L1: diversity  $\sim 3.4 \times 10^3$**

28	29	30	31	32
RDT	RTT	RVW	ANW	THT
D	I	D	I	F
G	V	E	K	S
I		G	N	Y
N		K	R	
S		N	S	
V		S	T	
		T	V	

**CDR-L2: diversity = 18**

50	53
KBG	AVC
A	N
G	S
L	T
S	
V	
W	

**CDR-L3: diversity  $\sim 1.0 \times 10^4$**

91	92	93	94	96
KMT	DMC	RVT	NHT	YHT
A	A	A	A	F
D	D	D	D	H
S	N	G	F	L
Y	S	N	H	P
	T	S	I	S
	Y	Y	L	T
			N	N
			P	P
			S	S
			T	T
			V	V
			Y	Y

**FIG.-** 38

**Light Chain Designed Diversity****CDR-L3: diversity  $\sim 1.3 \times 10^3$** 

	91	92	93	94	96
TMT	DMC	RVT	WHT	HHT	
S	A	A	F	F	
Y	D	D	I	I	
N	G	N		L	
S	N	S			
T	S	T			
Y	T	Y			

**CDR-L1**

	28	29	30	31	32
	RDT	RTT	RVW	RVW	DHT
	D	I	D	D	A
	G	V	E	E	D
	I		G	G	
	N		K	K	
	S		N	N	
	V		S	S	
			T	T	
			V	V	

**FIG.- 39****CDR-L2**

	50	53
DVK	AVM	
A	N	
G	K	
L	R	
S	S	
V	T2	
W		

**CDR-L3**

	91	92	93	94	96
NRT	NRT	RVM	NNK	TDK	
C	C	A2	A	C	
D	D	D	C	F	
G	G	E	D	L	
H	H	G2	E	W	
N	N	K	F	Y	
R	R	N	G	*	
S	S	R	H		
Y	Y	S	I		
			T2		
				M	
				N	
				P	
				Q	
				R	
				etc	
				*	

\*Amber stop codon is encoded by the  
degenerate codon

**FIG.- 40**

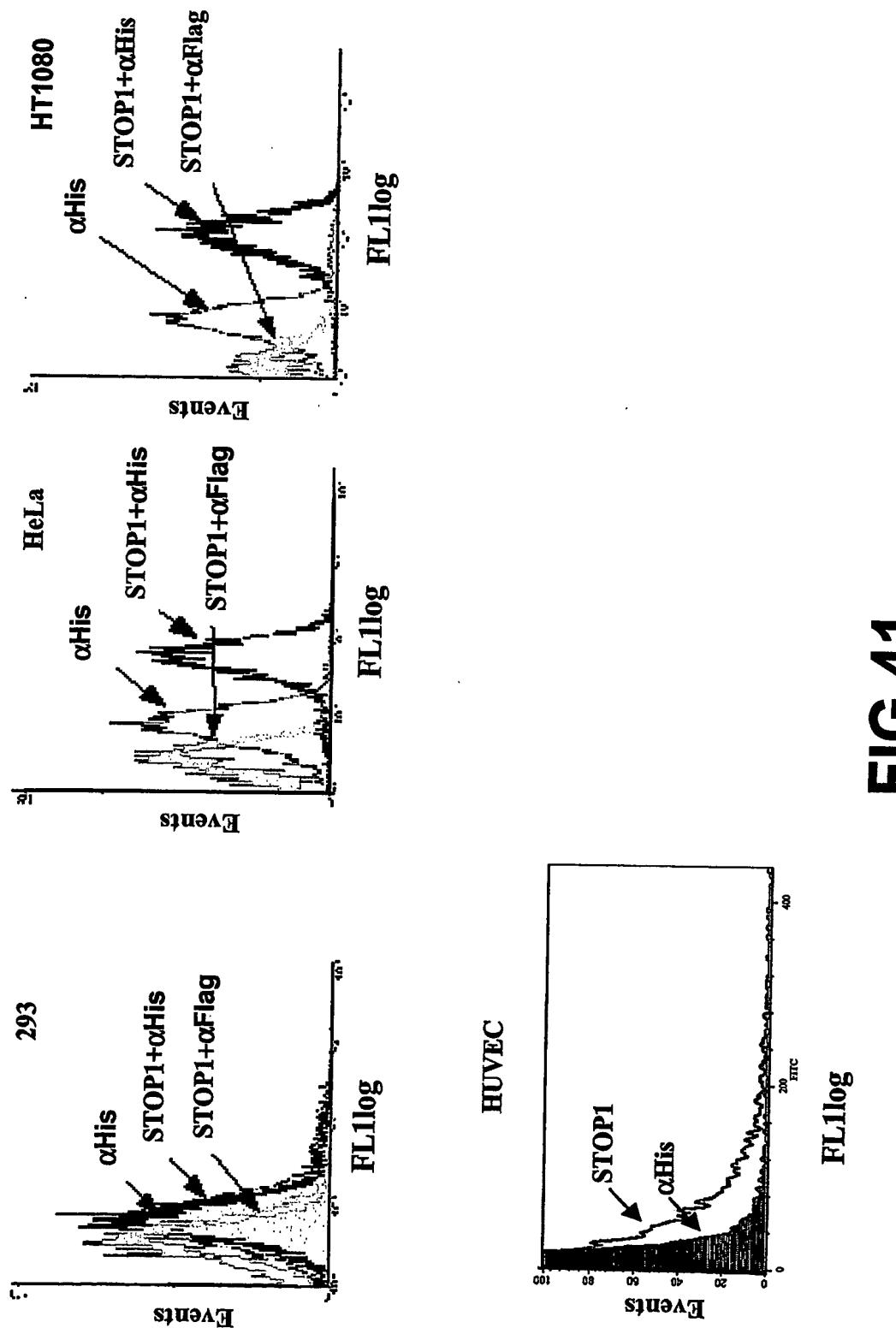


FIG.41

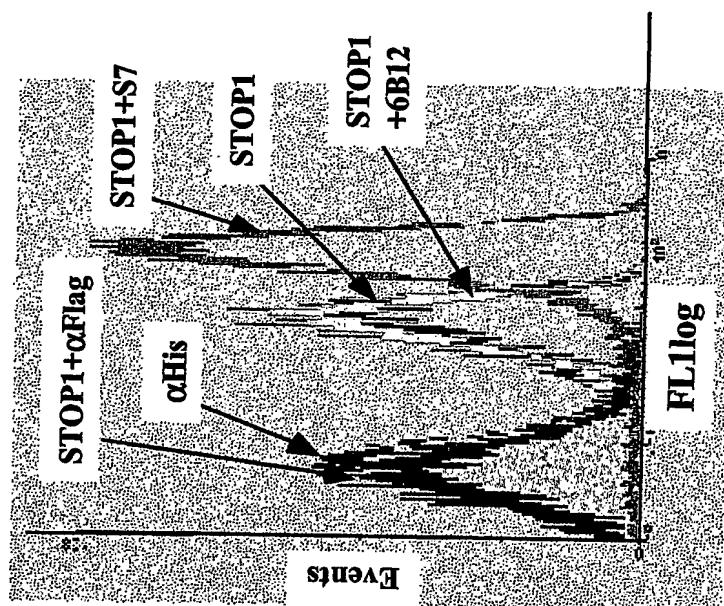


FIG.42

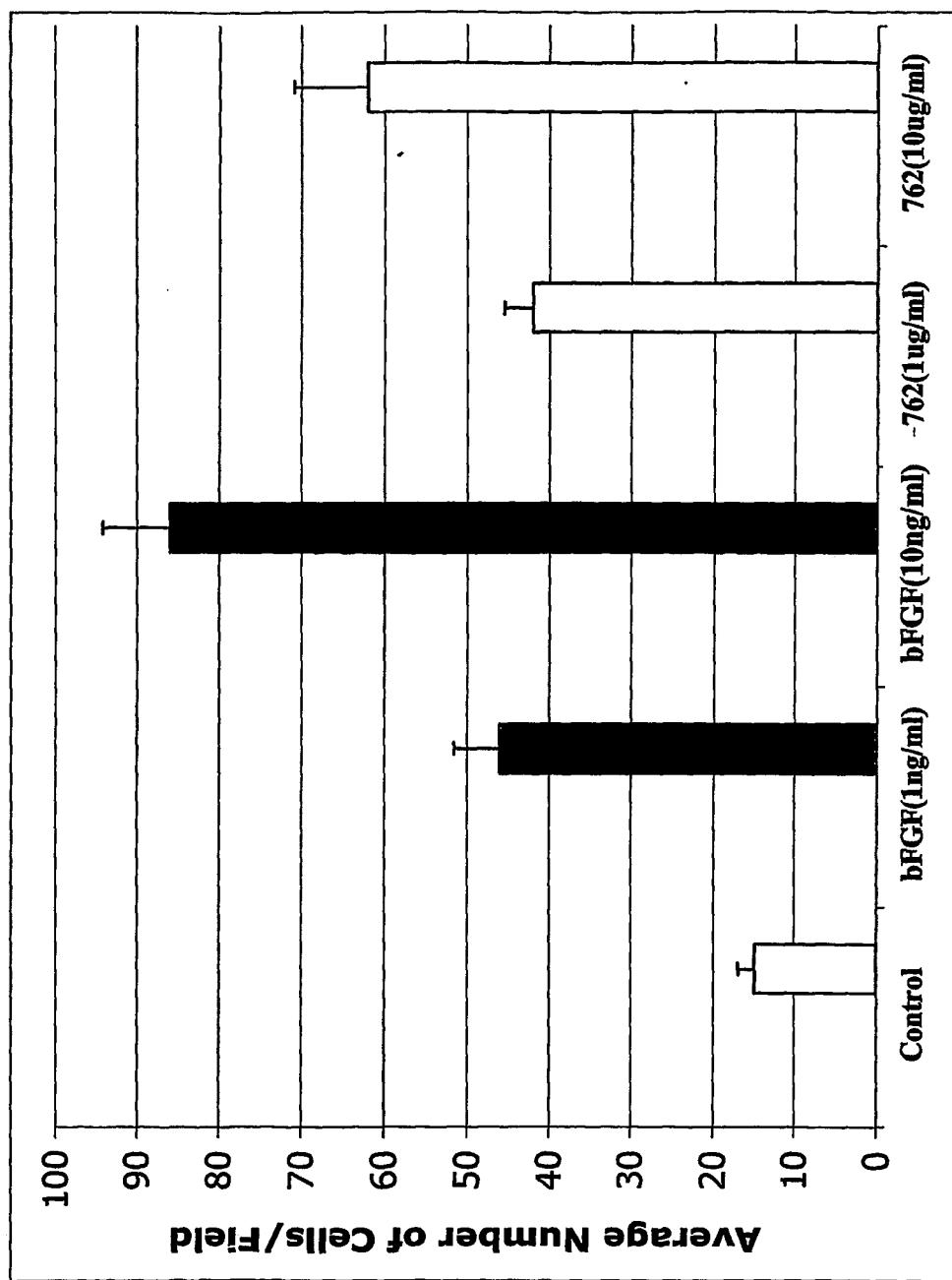


FIG.43

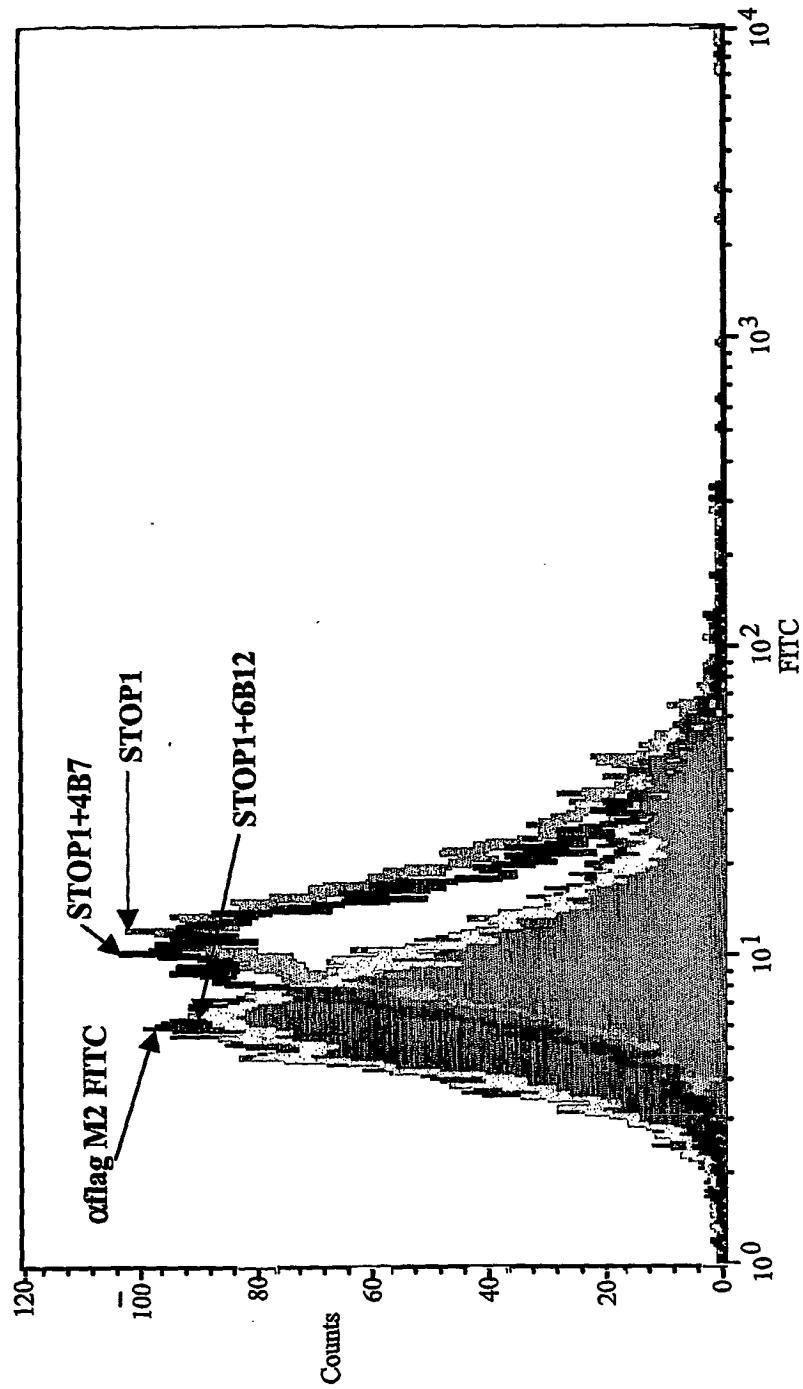
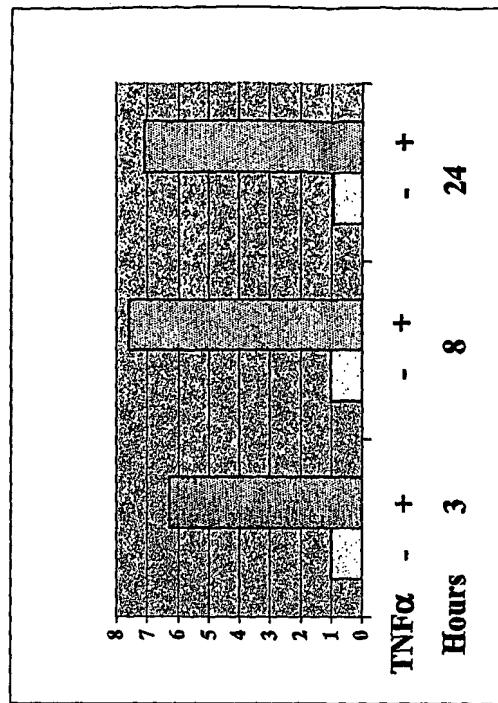
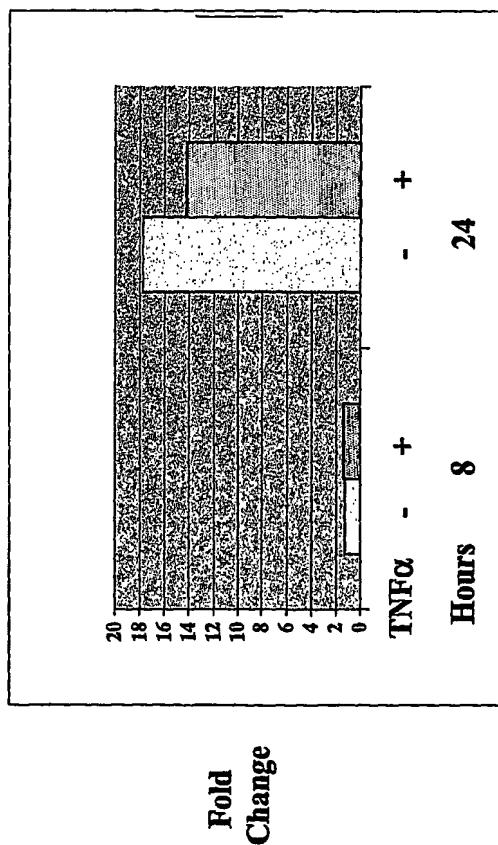


FIG.44

B.

**FIG.45**

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